

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 16, 2005, 08:21:09 ; Search time 496 Seconds
(without alignments)
256.679 Million cell updates/sec

Title: US-10-822-254-6
Perfect score: 554
Sequence: 1 SQIPASEQETLVKPKLLK.....NLVVNQSSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	Pending Patents AA Main:*
1:	/cgn2_6/ptodata/1/paa/PCTUS COMB.pep.*
2:	/cgn2_6/ptodata/1/paa/US06 COMB.pep.*
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27:	/cgn2_6/ptodata/1/paa/US101 COMB.pep.*
28:	/cgn2_6/ptodata/1/paa/US102 COMB.pep.*
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30:	/cgn2_6/ptodata/1/paa/US104 COMB.pep.*
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37:	/cgn2_6/ptodata/1/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	554	100.0	109	34	US-10-822-254-6	Sequence 6, Appli
2	551	99.5	109	34	US-10-822-254-10	Sequence 10, Appli
3	548	98.9	109	22	US-09-791-537-88970	Sequence 2, Appli
4	548	98.9	109	34	US-10-822-254-2	Sequence 2, Appli
5	548	98.9	138	21	US-09-724-676-50031	Sequence 50031, A
6	548	98.9	138	21	US-09-724-676-50032	Sequence 50032, A
7	548	98.9	138	21	US-09-724-676A-50031	Sequence 50031, A
8	548	98.9	138	21	US-09-724-676A-50032	Sequence 50032, A
9	548	98.9	209	21	US-09-724-676-50030	Sequence 50030, A
10	548	98.9	209	21	US-09-724-676A-50030	Sequence 50030, A
11	548	98.9	253	35	US-10-990-328-10898	Sequence 10898, A
12	548	98.9	253	37	US-60-505-218-571	Sequence 571, App
13	548	98.9	491	1	PCT-US01-19988-1	Sequence 1, Appli
14	548	98.9	491	1	PCT-US02-29780-8	Sequence 8, Appli
15	548	98.9	491	1	PCT-US03-12946-2602	Sequence 2602, Ap
16	548	98.9	491	1	PCT-US03-34636-22	Sequence 22, Appli
17	548	98.9	491	1	PCT-US03-38193-2236	Sequence 2236, Ap
18	548	98.9	491	1	PCT-US04-12347-1	Sequence 1, Appli
19	548	98.9	491	7	US-08-390-474-2	Sequence 2, Appli
20	548	98.9	491	7	US-08-390-516-2	Sequence 2, Appli
21	548	98.9	491	7	US-08-390-516B-3	Sequence 3, Appli
22	548	98.9	491	7	US-08-390-517-2	Sequence 2, Appli
23	548	98.9	491	7	US-08-390-789-2	Sequence 2, Appli
24	548	98.9	491	14	US-09-029-327-2	Sequence 15, Appli
25	548	98.9	491	19	US-09-587-473-15	Sequence 258, App
26	548	98.9	491	22	US-09-791-537-258	Sequence 1, Appli
27	548	98.9	491	23	US-09-888-077-1	Sequence 4, Appli
28	548	98.9	491	24	US-09-936-035-4	Sequence 8, Appli
29	548	98.9	491	25	US-09-956-425-8	Sequence 2, Appli
30	548	98.9	491	25	US-09-966-724-2	Sequence 2, Appli
31	548	98.9	491	25	US-09-966-724A-2	Sequence 3, Appli
32	548	98.9	491	25	US-09-966-724B-3	Sequence 7482, Ap
33	548	98.9	491	25	US-10-219-051B-7482	Sequence 18, Appli
34	548	98.9	491	28	US-10-228-218A-18	Sequence 35, Appli
35	548	98.9	491	28	US-10-232-951-35	Sequence 137, App
36	548	98.9	491	30	US-10-422-536-137	Sequence 28, Appli
37	548	98.9	491	30	US-10-422-807-28	Sequence 8, Appli
38	548	98.9	491	32	US-10-489-802-8	Sequence 2, Appli
39	548	98.9	491	32	US-10-608-463-2	Sequence 1, Appli
40	548	98.9	491	32	US-10-685-838-1	Sequence 2236, Ap
41	548	98.9	491	33	US-10-723-860-2236	Sequence 2, Appli
42	548	98.9	491	33	US-10-724-225-2	Sequence 31187, A
43	548	98.9	497	27	US-10-170-205B-31187	Sequence 10897, A
44	548	98.9	497	35	US-10-990-328-10897	Sequence 132, App
45	548	98.9	497	37	US-60-449-629-132	

ALIGNMENTS

RESULT 1
US-10-822-254-6
; Sequence 6, Application US/10822254
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Duca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787

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Rooke
10/822254 Page 1
Seq. 10 6 w/ hter

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; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-254-6

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	Query Match	100.0%	Score 554;	DB 34;	Length 109;
	Best Local Similarity	100.0%;	Pred. No. 3.8e-59;		
	Matches 109;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SQIPASEQETLVRPKPLLLLLLKLSVGAQDKDTYTMKEVLFYLGQYIMTKRLDYDEKQOIHV	60		
Db	1	SQIPASEQETLVRPKPLLLLLLKLSVGAQDKDTYTMKEVLFYLGQYIMTKRLDYDEKQOIHV	60		
Qy	61	CSNLLIGDLFCVPSPFSVKEHKRYITMIYRNLVVNNQOESSDSGTSVSEN	109		
Db	61	CSNLTIGDLFCVPSPFSVKEHKRYITMIYRNLVVNNQOESSDSGTSVSEN	109		

RESULT 2
US-10-822-254-10
: Sequence 10. Application US/10822254

Query Match	99.5%	Score 551;	DB 34;	Length 109;
Best Local Similarity	99.1%	Pred. No. 8.9e-59;		
Matches 108;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SQIPASQEITLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVH	60	
		IQIPASQEITLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVH		
Db	1	SQIPASQEITLVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVH	60	
Qy	61	CSNDLLGLDLCVPSPFSVKEHRKITYMTLYRNLVVVNOQESSDSGTSVSEN	109	
Db	61	CSNDLLGLDLCVPSPFSVKEHRKITYMTLYRNLVVVNOQESSDSGTSVSEN	109	

RESULT 3
US-09-791-537-88970
; Sequence 88970, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek

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; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88970
; LENGTH: 109
; TYPE: PRT
; ORGANISM: pdb LYCRA
; US-09-791-537-88970

      Query Match          98.9%;      Score 548;      DB 22;      Length 109;
      Best Local Similarity 99.1%;      Pred. No. 2.1e-58;
      Matches 108;      Conservative 1;      Mismatches 0;      Indels 0;      Gaps 0;

QY      1      SQIPASEQETLVKRPKLLKLLKLLKLVGAQKDYTYMKVELFYLGQYIMTKRLYDEKQOHLVH 60
Db      1      SQIPASEQETLVKRPKLLKLLKLLKLVGAQKDYTYMKVELFYLGQYIMTKRLYDEKQOHLVY 60

QY      61      CSNDLLGLDGLFGVPSFSVKEHKRIYTMIVRNLVVNNQESSDSGTSVSEN 109
Db      61      CSNDLLGLDGLFGVPSFSVKEHKRIYTMIVRNLVVNNQESSDSGTSVSEN 109

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RESULT 4
US-10-822-254-2
; Sequence 2, Application US/10822254
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Duca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 109
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-822-254-2

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	Query Match	98.9%	Score 548;	DB 34;	Length 109;
	Best Local Similarity	99.1%	Pred. No. 2.1e-58;		
	Matches 108; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SQIPASEQEETLVRPKPELLLLKLSVGAQDXTYTMKEVLFYLGQYIMTKRLYDEKQOHHV	60		
Db	1	SQIPASEQEETLVRPKPELLLLKLSVGAQDXTYTMKEVLFYLGQYIMTKRLYDEKQOHHV	60		
QY	61	CSNDLLGDLFGVPFSFGVCKHRKIYTIMYRNLLVVNQOESSDSTSVSEN	109		
Db	61	CSNDLLGDLFGVPFSFGVCKHRKIYTIMYRNLLVVNQOESSDSTSVSEN	109		

RESULT 5
US-09-724-676-50031
; Sequence.50031, Application US/09724676

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; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50031
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50031

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 125

RESULT 6
US-09-724-676-50032
; Sequence 50032, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50032
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50032

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 125

RESULT 7
US-09-724-676-50031
; Sequence 50031, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50031
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50031

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 125

RESULT 8
US-09-724-676A-50032
; Sequence 50032, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50032
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-50032

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 125

RESULT 9
US-09-724-676-50030
; Sequence 50030, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50030
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50030

Query Match      98.9%; Score 548; DB 21; Length 209;
Best Local Similarity 99.1%; Pred. No. 5.1e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 83 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 131
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RESULT 10
US-09-724-676A-50030
; Sequence 50030, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50030
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-50030

Query Match          98.9%; Score 548; DB 21; Length 209;
Best Local Similarity 99.1%; Pred. No. 5.1e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

QY 61 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 109
Db 83 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 131

- RESULT 11
US-10-990-328-10898
; Sequence 10898, Application US/10990328
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CLO01495
; CURRENT APPLICATION NUMBER: US/10/990,328
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10898
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328-10898

Query Match          98.9%; Score 548; DB 35; Length 253;
Best Local Similarity 99.1%; Pred. No. 6.6e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

QY 61 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 109
Db 83 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 131

- RESULT 12
US-60-505-218-571
; Sequence 571, Application US/60505218
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CANCER, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01482
; CURRENT APPLICATION NUMBER: US/60/505,218
; CURRENT FILING DATE: 2003-09-24
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; NUMBER OF SEQ ID NOS: 22507
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-505-218-571

Query Match          98.9%; Score 548; DB 37; Length 253;
Best Local Similarity 99.1%; Pred. No. 6.6e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

QY 61 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 109
Db 83 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 131

- RESULT 13
PCT-US01-19988-1
; Sequence 1, Application PC/TUS0119988
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: PCT/US01/19988
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19988-1

Query Match          98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 109
Db 77 CSNDLLGDLFGVPFSFVKHHRKIYTMIRNLVVVNQOESSDGSSTSVSEN 125

- RESULT 14
PCT-US02-29780-8
; Sequence 8, Application PC/TUS0229780
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
; TITLE OF INVENTION: Method of Use Thereof
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: PCT/US02/29780
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/956,425
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 491
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TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-29780-8

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGLDGLFGVPSPSVKXEHRIYTMIVRNLVVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGLDGLFGVPSPSVKXEHRIYTMIVRNLVVNVNQESSDSGTSVSEN 125

RESULT 15

PCT-US03-12946-2602
Sequence 2602, Application PC/TUS0312946
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000150
CURRENT APPLICATION NUMBER: PCT/US03/12946
CURRENT FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,827
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2602
LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-12946-2602

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGLDGLFGVPSPSVKXEHRIYTMIVRNLVVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGLDGLFGVPSPSVKXEHRIYTMIVRNLVVNVNQESSDSGTSVSEN 125

Search completed: February 16, 2005, 08:36:52
Job time : 498 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	311.5	56.2	205	6	US-10-450-763-60317	Sequence 60317, A
2	246	44.4	140	6	US-10-499-353A-580	Sequence 580, App
3	246	44.4	148	6	US-10-499-353A-585	Sequence 585, App
4	246	44.4	343	6	US-10-499-353A-584	Sequence 584, App
5	225	40.6	107	6	US-10-499-353A-581	Sequence 581, App
6	184	33.2	361	6	US-10-450-763-60315	Sequence 60315, A
7	176	31.8	243	5	US-09-786-702-2	Sequence 2, Appli
8	161	29.1	74	6	US-10-450-763-60316	Sequence 60316, A
9	75	13.5	254	6	US-10-450-763-60313	Sequence 60313, A
10	74.5	13.4	236	1	PCR-1B03-06509-5659	Sequence 5659, Ap
11	73.5	13.3	621	6	US-10-450-763-55457	Sequence 55457, A
12	71	12.8	473	8	US-60-643-717-5118	Sequence 5118, Ap
13	71	12.8	473	8	US-60-643-717-15695	Sequence 15695, A
14	70.5	12.7	787	6	US-10-450-763-55458	Sequence 55458, A
15	69	12.5	291	7	US-11-031-175-15646	Sequence 15646, A
16	66.5	12.0	422	8	US-60-643-717-2338	Sequence 2338, Ap
17	66	11.9	2228	6	US-10-450-763-39401	Sequence 39401, A
18	66	11.9	2275	6	US-10-489-448-1766	Sequence 1766, Ap
19	64	11.6	478	1	PCR-US04-20180-30	Sequence 30, Appl
20	64	11.6	971	6	US-10-450-763-36645	Sequence 36645, A
21	63.5	11.5	598	6	US-10-450-763-52598	Sequence 52598, A
22	63	11.4	435	6	US-10-450-763-39688	Sequence 39688, A
23	63	11.4	533	6	US-10-450-763-39487	Sequence 39487, A
24	62.5	11.3	355	8	US-60-643-717-12981	Sequence 12981, A
25	62.5	11.3	445	6	US-10-450-763-45047	Sequence 45047, A

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; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 580
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-580

Query Match          44.4%; Score 246; DB 6; Length 140;
Best Local Similarity 55.4%; Pred. No. 8.3e-22;
Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAQQEMFTVKEVMHYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIYTYMYRNLVV 94
Db 87 RQSFVKDPSPLYDMLRKNLVT 109

RESULT 3
US-10-499-353A-585
; Sequence 585, Application US/10499353A
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 585
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-585

Query Match          44.4%; Score 246; DB 6; Length 148;
Best Local Similarity 55.4%; Pred. No. 8.9e-22;
Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAQQEMFTVKEVMHYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIYTYMYRNLVV 94
Db 87 RQSFVKDPSPLYDMLRKNLVT 109

RESULT 4
US-10-499-353A-584
; Sequence 584, Application US/10499353A
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
```

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; CURRENT APPLICATION NUMBER: US/10/499,353A
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 584
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-584

Query Match          44.4%; Score 246; DB 6; Length 343;
Best Local Similarity 55.4%; Pred. No. 2.4e-21;
Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAQQEMFTVKEVMHYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIYTYMYRNLVV 94
Db 87 RQSFVKDPSPLYDMLRKNLVT 109

RESULT 5
US-10-499-353A-581
; Sequence 581, Application US/10499353A
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 581
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-581

Query Match          40.6%; Score 225; DB 6; Length 107;
Best Local Similarity 57.5%; Pred. No. 1.8e-19;
Matches 42; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAQQEMFTVKEVMHYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIY 84
Db 87 RQSFVKDPSPLY 99

RESULT 6
US-10-450-763-60315
; Sequence 60315, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
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US-10-450-763-60315 ; OTHER INFORMATION: 40.6

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; Sequence 60313, Application US/10450/763
;
; GENERAL INFORMATION:
;
; APPLICANT: Hyseq, Inc
;
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;
; FILE REFERENCE: 790CIP3/US
;
; CURRENT APPLICATION NUMBER: US/10/450,763
;
; CURRENT FILING DATE: 2003-06-11
;
; PRIORITY APPLICATION NUMBER: PCT/US01/08631
;
; PRIOR FILING DATE: 2001-03-30
;
; PRIOR APPLICATION NUMBER: 09/540,217
;
; PRIOR FILING DATE: 2000-03-31
;
; PRIOR APPLICATION NUMBER: 09/649,167
;
; PRIOR FILING DATE: 2000-08-23
;
; NUMBER OF SEQ ID NOS: 60736
;
; SOFTWARE: Custom
;
; SEQ ID NO 60313
;
; LENGTH: 254

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/ PRIOR APPLICATION NUMBER: 05/350,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 60313
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(254)
/ OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-60313

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[illegible]

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Db      238 DLSIRE--LYISNYITL 252
RESULT 10
PCT-IB03-06509-5659
; Sequence 5659, Application PC/TIB0306509
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota and The United States of A
; APPLICANT: Secretary of Agriculture
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09531/112W01
; CURRENT APPLICATION NUMBER: PCT/IB03/06509
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/137,113
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/362,396
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 5809
; SOFTWARE: FAST-SEQO for Windows Version 4.0

```

10


```

; OTHER INFORMATION: accession number PR00690A, p-value=9.866e-09, raw score of 10.86
US-10-450-763-55458

Query Match      12.7%; Score 70.5; DB 6; Length 787;
Best Local Similarity 25.5%; Pred. No. 3.1;
Matches 25; Conservative 19; Mismatches 33; Indels 21; Gaps 3;

QY 1 SQIPASEQ-----ETLVRPKPLLLKLLXSVG---AQKDTYTMKEVLFYLGQYIMTKRLYDE 53
Db 598 STVLASVQRTAGTEQMEPEQSAIMQAFQSGFLQPDHLFXQNLFYLETTLNTKOKLYHK 657

QY 54 K-----QQHIVHCSNDLLGLDFGVPSFSV 77
Db 658 KIFRTAMLFQFVNVLQVLVHKSHDLQBEIGIAYNM 695

RESULT 15
US-11-031-175-15646
; Sequence 15646, Application US/11031175
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/11/031,175
; CURRENT FILING DATE: 2005-01-08
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15646
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(291)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-031-175-15646

Query Match      12.5%; Score 69; DB 7; Length 291;
Best Local Similarity 25.8%; Pred. No. 1.4;
Matches 23; Conservative 23; Mismatches 23; Indels 20; Gaps 6;

QY 11 LVRPKPLLLKLL---KSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVHCSNDLLG 67
Db 100 LTRYFPPLSPYLVHGLTGAR-----MKVMAFMGPYVLPEDV-EERTEHVH----LVA 148

QY 68 DLFGVPFSVKE---HRKI---YTWIYRN 90
Db 149 GSGAVPNFAILKDALHRLGLKRLHTFLFSN 177

Search completed: February 16, 2005, 08:38:20
Job time : 84 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 166 Seconds
(without alignments)
253.957 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETVLRKPKLLK.....NLVVNQESDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	98.9	284	2 AAR75494	Aar75494 Human dou
2	548	98.9	284	2 AAR75397	Aar75397 Human dou
3	548	98.9	491	2 AAR42175	Aar42175 Human MDM
4	548	98.9	491	2 AAR76696	Aar76696 Human MDM
5	548	98.9	491	2 AAR70787	Aar70787 Human MDM
6	548	98.9	491	2 AAW15463	AAW15463 Human MDM
7	548	98.9	491	2 AAW13380	AAW13380 Human MDM
8	548	98.9	491	2 AAW13600	AAW13600 Murine do
9	548	98.9	491	2 AAW48241	AAW48241 Human MDM
10	548	98.9	491	2 AAW57241	AAW57241 Human MDM
11	548	98.9	491	2 AAW42879	AAW42879 Amino aci
12	548	98.9	491	2 AAW42971	AAW42971 Amino aci
13	548	98.9	491	2 AAW94304	AAW94304 Human MDM
14	548	98.9	491	3 AAY96567	AAY96567 MDM2 onco
15	548	98.9	491	4 AAB48284	AAB48284 Human MDM
16	548	98.9	491	5 AAE22654	AAE22654 Human Rin
17	548	98.9	491	5 AAE22698	AAE22698 Human Rin
18	548	98.9	491	5 AAE25913	AAE25913 Human dou
19	548	98.9	491	5 AAO15376	AAO15376 Human Dm2
20	548	98.9	491	7 ADD21815	ADD21815 Human mdm
21	548	98.9	491	7 ADE61562	ADE61562 Human Pro
22	548	98.9	491	8 ADL23893	ADL23893 Human p53
23	548	98.9	491	8 ADO52353	ADO52353 Human p53
24	548	98.9	491	8 ADP12593	ADP12593 Protein e
25	548	98.9	491	8 ADN71936	ADN71936 MDM2 prot

26	548	98.9	491	8 ADO19417	Adg19417 Human sof
27	548	98.9	491	8 ADR58893	Adr58893 Human MDM
28	548	98.9	1171	4 AAU32421	AAU32421 Novel hum
29	531.5	95.9	216	3 AAB08846	AAB08846 A human M
30	522.5	94.3	522	7 ADJ95152	Adj95152 Novel NOV
31	522.5	94.3	522	7 ADJ95154	Adj95154 Novel NOV
32	488.5	88.2	489	2 AAR42176	Aar42176 Murine MD
33	488.5	88.2	489	2 AAR76697	Aar76697 Mouse MDM
34	488.5	88.2	489	2 AAW07888	Aaw07888 Murine MD
35	488.5	88.2	489	2 AAW15464	Aaw15464 Murine MD
36	488.5	88.2	489	2 AAW48242	Aaw48242 Mouse MDM
37	488.5	88.2	489	2 AAW57246	Aaw57246 Mouse MDM
38	488.5	88.2	489	2 AAW42997	Aaw42997 Amino aci
39	488.5	88.2	489	2 AAW42972	Aaw42972 Amino aci
40	488.5	88.2	489	2 AAW94305	Aaw94305 Mouse MDM
41	488.5	88.2	489	5 AAE25914	Aae25914 Mouse dou
42	488.5	88.2	489	5 ABB57099	Abb57099 Mouse lsc
43	488.5	88.2	489	5 AAO15375	Aao15375 Mouse Dm2
44	488.5	88.2	489	7 ADD21816	Add21816 Mouse mdm
45	488.5	88.2	489	7 ADE61560	Ade61560 Rat Prote

ALIGNMENTS

RESULT 1
ID AAR75494 standard; protein; 284 AA.
XX AAR75494;
AC AAR75494;
XX
XX
DT 02-FEB-1996 (first entry)
XX
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 1..284
FT /note= "amino acids 1-284 of hdm-2 gene product"
XX
XX
FN DE4339533-A1.
XX
XX
PD 14-JUN-1995.
XX
XX
PF 19-NOV-1993; 93DE-04339533.
XX
XX
PR 19-NOV-1993; 93DE-04339533.
XX
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
XX
DR WPI; 1995-216248/29.
XX
XX
DR N-PSDB; AAQ92515.
XX
XX
PT Detection of human double minute gene 2 (hdm-2) antibodies - by
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in
PT the detection of specific cancers.
XX
XX
PS Claim 11; Fig 1; 12pp; German.
XX
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies in a claimed immunoassay method.
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of
CC cancer, e.g. rhabdomyosarcoma
XX
XX
SQ Sequence 284 AA;


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AC AAW15463;
XX
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
XX Human MDM2.
DE
XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;
XX p53-regulated growth.
KW
XX Homo sapiens.
OS
XX
XX US5618921-A.
FN
XX
XX 08-APR-1997.
PD
XX
XX 17-FEB-1995; 95US-00390479.
PF
XX
XX 07-APR-1992; 92US-00867840.
PR
XX 23-JUN-1992; 92US-00903103.
PR
XX 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
PI
XX
XX WPI; 1997-225474/20.
DR
XX N-PSDB; AAT66410.
DR
XX
XX Antibodies specific for human MDM2 protein - for diagnosis of cancer.
PT
XX
XX Claim 1; Col 19-24; 35pp; English.
PS
XX
XX This sequence represents the human MDM2 protein. Antibodies that
CC specifically bind to human MDM2 protein may be used for detecting
CC elevated expression of the MDM2 gene in a human tissue or body fluid
CC sample, esp. for cancer diagnosis. The antibodies may be used to
CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC to sequester p53 and allow the cell to escape from p53-regulated growth.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125
RESULT 7
AAW13380
ID AAW13380 standard; protein; 491 AA.
XX
XX AAW13380;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1997 (first entry)
XX
XX Human MDM2 protein.
DE
XX Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
XX Homo sapiens.
OS
XX

```

```

FN US5606044-A.
XX
XX 25-FEB-1997.
PD
XX
XX 17-FEB-1995; 95US-00390546.
PF
XX
XX 07-APR-1992; 92US-00867840.
PR
XX 23-JUN-1992; 92US-00903103.
PR
XX 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;
PI
XX
XX WPI; 1997-153623/14.
DR
XX N-PSDB; AAT62065.
DR
XX
XX Detection of amplification of human MDM2 gene - useful for diagnosis of
PT neoplasia or potential neoplastic transformation.
XX
XX Example 1; Col 21-24; 35pp; English.
PS
XX
XX The present sequence is the human MDM2 protein, the cDNA for which was
CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC the amplification or elevated expression of a human MDM2 gene, which is
CC diagnostic of neoplasia or the potential for neoplastic transformation,
CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125
RESULT 8
AAW13600
ID AAW13600 standard; protein; 491 AA.
XX
XX AAW13600;
AC
XX
XX 16-JAN-1998 (first entry)
DT
XX
XX Murine double minute 2 protein sequence.
DE
XX
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW restenosis.
XX
XX Mus musculus.
OS
XX
XX WO9709343-A2.
FN
XX
XX 13-MAR-1997.
PD
XX
XX 02-SEP-1996; 96WO-FR001340.
PF
XX
XX 04-SEP-1995; 95FR-00010331.
PR
XX
XX (RHON ) RHONE POULENC RORER SA.
PA

```


PA (INRM) INST NAT SANTE & RECH MEDICALE.
 XX
 XX Toocque B, Dubs-Peterszman M, Wasylyk B;
 XX
 XX WPI; 1997-192837/17.
 XX N-PSDB; AAT61637.
 DR
 DR Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
 PT or nucleic acid encoding an antagonist, also viral vectors contg. this
 PT nucleic acid.
 XX
 XX Claim 2; Page 26-30; 43pp; French.
 XX
 CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-
 CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity
 CC of the tumour suppressor protein p53. It has now been shown that the mdm2
 CC protein itself has oncogenic properties, especially in a p53-null
 CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by
 CC over-expression of the p107 protein. This is especially done by the
 CC region covering amino acid 1-134. The invention therefore relates to
 CC antagonists able to inhibit the oncogenic activity of mdm2. These include
 CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
 CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.
 CC TP11, TBP or TAP250, which bind amino acids 1-134 of mdm2. Other
 CC inhibitors include compounds which disrupt binding to region 135-491 of
 CC mdm2, e.g. RB, L5 or the transcription factor E2F. The antagonists are
 CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
 CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other
 CC hyperproliferative conditions such as restenosis
 XX
 XX Sequence 491 AA;
 SQ

Query Match 98.9%; Score 548; DB 2; Length 491;
 Best Local Similarity 99.1%; Pred. No. 7e-64;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
 DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109
 DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 9
 AAW48241
 ID AAW48241 standard; protein; 491 AA.
 XX
 XX AC AAW48241;
 XX
 DT 18-JUN-1998 (first entry)
 XX
 DE Human MDM2.
 XX
 KW Human; MDM2; tumour; cancer; diagnosis; neoplastic disease;
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
 XX
 OS Homo sapiens.
 XX
 FN US5736338-A.
 XX
 PD 07-APR-1998.
 XX
 PF 17-FEB-1995; 95US-00390517.
 XX
 PR 07-APR-1992; 92US-00867840.
 PR 23-JUN-1992; 92US-00903103.
 PR 07-APR-1993; 93US-00044619.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;
 XX

Query Match 98.9%; Score 548; DB 2; Length 491;
 Best Local Similarity 99.1%; Pred. No. 7e-64;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
 DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109
 DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 10
 AAW57241
 ID AAW57241 standard; protein; 491 AA.
 XX
 XX AC AAW57241;
 XX
 DT 10-AUG-1998 (first entry)
 XX
 DE Human MDM2 protein.
 XX
 KW Human; p53; MDM2; tumour; growth inhibition; amplification;
 KW malignant fibrous histiocytoma; liposarcoma.
 XX
 OS Homo sapiens.
 XX
 FN US5756455-A.
 XX
 PD 26-MAY-1998.
 XX
 PF 17-FEB-1995; 95US-00390515.
 XX
 PR 07-APR-1992; 92US-00867840.
 PR 23-JUN-1992; 92US-00903103.
 PR 07-APR-1993; 93US-00044619.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1998-321574/28.
 DR N-PSDB; AAV28876.
 XX
 PT Inhibiting growth of tumour cells having MDM2 gene amplification - with
 PT p53 protein fragment.
 XX
 PS Claim 1; Col 23-28; 40pp; English.
 XX
 CC A method has been developed for inhibiting the growth of tumour cells
 CC containing a human MDM2 gene amplification. The method comprises treating
 CC the tumour cells with a DNA molecule that expresses a polypeptide capable
 CC of binding to human MDM2 protein. The present sequence represents human
 CC MDM2 protein. The present invention describes three preferred
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino
 CC acids 13-41 of p53 (see AAW57240) and at least none additional p53
 CC residues on the N- or C-terminal side, provided that the polypeptide
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
 CC additional p53 residues on the N- or C-terminal side, provided that the
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so
 CC detection of increased expression of MDM2 gene products indicates
 CC tumourigenesis
 XX
 XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;
 Best Local Similarity 99.1%; Pred. No. 7e-64;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
 Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
 Qy 61 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
 Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 11
 AAW42879
 ID AAW42879 standard; protein; 491 AA.
 XX
 AC AAW42879;
 XX
 DT 30-APR-1998 (first entry)
 DE Amino acid sequence of human MDM2.
 XX
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
 KW binding; tumour cell; p53-regulated growth; inhibition;
 KW anti-cancer agent.
 XX
 OS Homo sapiens.
 XX
 FN US5708136-A.
 XX
 PD 13-JAN-1998.
 XX
 PF 17-FEB-1995; 95US-00390516.
 XX
 PR 07-APR-1992; 92US-00867840.
 PR 23-JUN-1992; 92US-00903103.
 PR 07-APR-1993; 93US-00044619.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
 PI
 DR WPI; 1998-100408/09.
 XX
 PT Human MDM2 binding polypeptide - comprises fragments of p53, useful in re
 PT -establishing p53-regulated growth control in cells over-expressing MDM2.
 XX
 XX Disclosure; Col 23-28; 41pp; English.

PS The present sequence represents human MDM2. The MDM2 gene is amplified in
 XX some human tumours. The amplification of this gene is diagnostic of
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a
 CC potential DNA binding protein that functions in the modulation of
 CC expression of other genes and, when present in excess, interferes with
 CC normal constraints on cell growth. A cell containing three recombinant
 CC DNA constructs was produced. These constructs encode an MDM2 protein
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 CC to a transcriptional activation domain, and a reporter gene downstream
 CC from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
 CC cells and since binding of MDM2 to p53 appears to allow tumour cells to
 CC escape from p53-regulated growth, compounds that inhibit such binding
 CC would be useful as anti-cancer agents
 XX
 XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;
 Best Local Similarity 99.1%; Pred. No. 7e-64;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
 Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
 Qy 61 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
 Db 77 CSNDLLGDLFGVPSFVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 12
 AAW42971
 ID AAW42971 standard; protein; 491 AA.
 XX
 AC AAW42971;
 XX
 DT 29-APR-1998 (first entry)
 DE Amino acid sequence of human MDM2.
 XX
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
 KW binding; tumour cell; p53-regulated growth; inhibition;
 KW anti-cancer agent.
 XX
 OS Homo sapiens.
 XX
 FN US702903-A.
 XX
 PD 30-DEC-1997.
 XX
 PF 13-NOV-1995; 95US-00557393.
 XX
 PR 07-APR-1992; 92US-00867840.
 PR 23-JUN-1992; 92US-00903103.
 PR 07-APR-1993; 93US-00044619.
 PR 18-MAY-1994; 94US-00245500.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Vogelstein B, Kinzler KW;
 PI
 DR WPI; 1998-076411/07.
 XX
 DR N-PSDB; AAV03607.
 XX
 PT Cell containing reporter construct containing human MDM2 and p53 genes -
 PT for identifying compounds that interfere with binding of human MDM2 to
 PT human p53, useful as anti-cancer agents.
 XX
 PS Disclosure; Coulms 22-28; 37pp; English.

XX The present sequence represents human MDM2. The MDM2 gene is amplified in
 CC some human tumours. The amplification of this gene is diagnostic of
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a
 CC potential DNA binding protein that functions in the modulation of
 CC expression of other genes and, when present in excess, interferes with
 CC normal constraints on cell growth. A cell containing three recombinant
 CC DNA constructs was produced. These constructs encode an MDM2 protein
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 CC to a transcriptional activation domain, and a reporter gene downstream
 CC from a DNA element which is recognised by the sequence-specific DNA-
 CC binding domain. The cell is used to identify a compound which interferes
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC escape from p53-regulated growth, compounds that inhibit such binding
CC would be useful as anti-cancer agents

SQ Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 109
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 125

RESULT 13
AAW94304
ID AAW94304 standard; protein; 491 AA.
AC AAW94304;
XX
DT 13-APR-1999 (first entry)
XX
DE Human MDM2.
XX
KW Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;
KW malignant fibrous histiocytoma; MFH; liposarcoma.
XX
OS Homo sapiens.
XX
PN US858976-A.
XX
PD 12-JAN-1999.
XX
PF 14-FEB-1997; 97US-00801718.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
PR 17-FEB-1995; 95US-00390515.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Kinzler KW, Vogelstein B;
XX
DR WPI; 1999-152105/13.
DR N-PSDB; AAX03947.

XX Inhibiting growth of tumour cells having MDM2 gene amplification - with
XX MDM2-binding p53 fragment.

PS Claim 1; Col 23-28; 4lpp; English.

XX The present invention describes: (1) a method for inhibiting the growth
XX of tumour cells which contain a human MDM2 gene amplification, comprising
XX administering to the cells a DNA molecule that expresses a polypeptide
XX consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
XX acid sequence given in AAW94303, the polypeptide being capable of binding
XX to human MDM2 (the present sequence); (2) a method as in (1) where the
XX polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
XX method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
XX The method is useful for treating the following tumour types which have a
XX MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20
XX MFH, L-9 liposarcoma, K17 liposarcoma, K128 liposarcoma, K130
XX liposarcoma, and OSA-CL MFH

SQ Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 109
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 125

RESULT 14
AAI96567
ID AAI96567 standard; protein; 491 AA.
AC AAI96567;
XX
DT 12-SEP-2000 (first entry)
XX
DE MDM2 oncoprotein.

XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW proliferation; immortal; tumour therapy; macular degeneration; activator;
KW INK4; MDM2; oncoprotein.
XX
OS Homo sapiens.
XX
PN WO200031238-A2.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US027907.
XX
PR 25-NOV-1998; 98US-0109891P.
PR 17-FEB-1999; 99US-0120549P.
XX
PA (GENE-) GENETICA INC.

XX Hannon GJ, Beach DH;
XX
DR WPI; 2000-400055/34.
DR N-PSDB; AAA29389.

XX New method for increasing the proliferative capacity of cell lines
XX comprises administering agents reversibly activating telomerase activity
XX and reversibly inactivating Rb/INK4 and/or p53 pathways useful in
XX treating age related diseases.

PS Claim 5; Page 120; 123pp; English.

XX The invention concerns methods and reagents for extending the life-span,
XX e.g. the number of mitotic divisions, of a cell. The method relies on
XX activation of a telomerase activity and inhibition of one or both of a
XX retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
XX by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
XX division cycle. Binding of INK4 family members, e.g. the tumour
XX suppressor p16INK4a, inhibits kinase activity and results in growth
XX arrest. Rb inactivators can selectively and reversibly inactivate an
XX Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
XX is a cellular inhibitor of Rb/p53 function and the p53 tumour suppressor
XX and can also be used in the methods. Other molecules which can be used
XX include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
XX differs from at one or more of residues K22, R24, H95 and/or D97.
XX Additional constructs include a papilloma virus E7 protein, or other
XX viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
XX the Rb and p16INK4a genes may also be used. The methods are useful for
XX increasing the proliferative capacity of cells. The cells are
XX subsequently of use in pharmaceutical and cosmetic preparations used to
XX treat conditions related to (premature) ageing, e.g. macular degeneration
XX and arteriosclerosis. The cells can also be used to replace tumour cell
XX lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be
CC of use in the production of normal or genetically engineered
CC biotechnology products
XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 3; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGFVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
DB 77 CSNDLLGLDGFVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

RESULT 15
AAB48284
ID AAB48284 standard; protein; 491 AA.

AC AAB48284;

DT 02-APR-2001 (first entry)

DE Human MDM2 protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2P;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytostatic.

OS Homo sapiens.

XX WO2000075184-A1.

PD 14-DEC-2000.

PF 05-JUN-2000; 2000WO-US015449.

PR 04-JUN-1999; 99US-0137494P.

XX (UYVA) UNIV YALE.

PI Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

DR N-PSDB; AAC84596.

XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins.

PS Claim 5; Page 93-95; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
CC cell, using proteins selected from S-phase kinase associated proteins 1
CC and 2 (SKP1, SKP2), SKP2-like proteins (2P) and CUL-1 (a member of the
CC cullin/CDC53 family of proteins). The method is useful for altering the
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC that modulate interactions between SKP and target proteins are useful for
CC treating tumours

XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 4; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGLDGFVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 109
DB 77 CSNDLLGLDGFVPSFSVKEHRKIYTMIRNLVVVNQOESSDSGTSVSEN 125

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OM protein - protein search, using sw model

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(without alignments)
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Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	98.9	188	4	US-09-603-052-4
2	548	98.9	491	1	US-07-903-103-2
3	548	98.9	491	1	US-08-044-619A-2
4	548	98.9	491	1	US-08-283-911-2
5	548	98.9	491	1	US-08-245-500A-3
6	548	98.9	491	1	US-08-390-546-3
7	548	98.9	491	1	US-08-479A-3
8	548	98.9	491	1	US-08-557-393-3
9	548	98.9	491	1	US-08-390-516C-3
10	548	98.9	491	1	US-08-390-517A-3
11	548	98.9	491	1	US-08-390-515A-3
12	548	98.9	491	2	US-08-801-718-3
13	548	98.9	491	3	US-09-170-159A-3
14	548	98.9	491	4	US-09-480-718-4A
15	548	98.9	528	4	US-09-949-016-7125
16	548	98.9	528	4	US-09-949-016-7126
17	548	98.9	528	4	US-09-949-016-7127
18	548	98.9	528	4	US-09-949-016-7128
19	548	98.9	528	4	US-09-949-016-7129
20	531.5	95.9	216	3	US-09-510-252-4
21	488.5	88.2	489	1	US-07-903-103-4
22	488.5	88.2	489	1	US-08-044-619A-4
23	488.5	88.2	489	1	US-08-283-911-4
24	488.5	88.2	489	1	US-08-245-500A-5
25	488.5	88.2	489	1	US-08-546-5
26	488.5	88.2	489	1	US-08-390-479A-5
27	488.5	88.2	489	1	US-08-557-393-5

28	488.5	88.2	489	1	US-08-390-516C-5
29	488.5	88.2	489	1	US-08-390-517A-5
30	488.5	88.2	489	1	US-08-390-515A-5
31	488.5	88.2	489	2	US-08-801-718-5
32	488.5	88.2	489	3	US-09-170-159A-5
33	488.5	88.2	489	4	US-09-480-718-46
34	244	44.0	490	4	US-09-949-016-6218
35	161	29.1	365	4	US-09-949-016-11388
36	71.5	12.9	420	4	US-09-270-767-43304
37	69.5	12.5	244	4	US-09-543-681A-6675
38	69	12.5	291	4	US-09-902-540-15646
39	68	12.3	766	4	US-09-248-796A-16626
40	67	12.1	2938	5	PCT-US94-00198-3
41	65	11.7	62	4	US-09-248-796A-24446
42	65	11.7	384	4	US-08-504-617-2
43	64	11.6	310	4	US-09-408-020-44
44	64	11.6	354	4	US-09-198-452A-317
45	64	11.6	354	4	US-09-438-185A-305

ALIGNMENTS

RESULT 1

US-09-603-052-4
; Sequence 4, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
; FILE REFERENCE: MEWB26.001C1
; CURRENT APPLICATION NUMBER: US/09/603,052
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: EP 95810576.9
; PRIOR FILING DATE: 1995-09-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03957
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-603-052-4

Query Match	98.9%	Score	548	DB	4	Length	188
Best Local Similarity	99.1%	Pred. No.	5.4e-61	Mismatches	0	Indels	0
Matches	108	Conservative	1	Indels	0	Gaps	0
QY	1	SOIPASEQETLVKPKLLKLSVGAQKDTVTMKEVLFYLGQYIMTKRLYDEKQOHVH	60				
Db	17	SOIPASEQETLVKPKLLKLSVGAQKDTVTMKEVLFYLGQYIMTKRLYDEKQOHVY	76				
QY	61	CSNDLLGLDFGVPSFVKHRIYTMVYRNLVVNQESSDSTSVSEN	109				
Db	77	CSNDLLGLDFGVPSFVKHRIYTMVYRNLVVNQESSDSTSVSEN	125				

RESULT 2

US-07-903-103-2
; Sequence 2, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.

```

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-903-103-2

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

US-07-903-103-2

RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103

; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-044-619A-2

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

US-08-044-619A-2

RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; LENGTH: 491 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-044-619A-2
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Db 77 CSNDLLGLDFGVPSFVSKHRKIYTIYRNLVVNNQOESSDGSITSVEN 125

RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,546
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-546-3

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLKLLKSGAOKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLKLLKSGAOKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIV 76

Qy 61 CSNDLLGLDFGVPSFVSKHRKIYTIYRNLVVNNQOESSDGSITSVEN 109
Db 77 CSNDLLGLDFGVPSFVSKHRKIYTIYRNLVVNNQOESSDGSITSVEN 125

RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390.479A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-390-479A-3

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVPRPKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHVH 60
Db 17 SQIPASEQETLVPRPKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHVH 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQSSDSGTSVSEN 125

RESULT 8
US-08-557-393-3
Sequence 3, Application US/08557393
Patent No. 5702903
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,393
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,500
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-393-3

Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVPRPKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHVH 60
Db 17 SQIPASEQETLVPRPKLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHVH 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNNQSSDSGTSVSEN 125

RESULT 9
US-08-390-516C-3
Sequence 3, Application US/08390516C
Patent No. 5708136
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,516C
FILING DATE: 07-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-390-516C-3

Query Match 98.9%; Score 548; DB 1; Length 491;
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 10

US-08-390-517A-3
 ; Sequence 3, Application US/08390517A
 ; Patent No. 5736338
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/390,517A
 ; FILING DATE: 07-APR-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 01107.42798
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-508-9100
 ; TELEFAX: 202-508-9299
 ; TELEX: 197430 BMB UT
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 491 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-390-517A-3

Query Match 98.9%; Score 548; DB 1; Length 491;
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 11

US-08-390-515A-3

; Sequence 3, Application US/08390515A
 ; Patent No. 5756455
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/390,515A
 ; FILING DATE: 07-APR-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 01107.42798
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-508-9100
 ; TELEFAX: 202-508-9299
 ; TELEX: 197430 BMB UT
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 491 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-390-515A-3

Query Match 98.9%; Score 548; DB 1; Length 491;
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 12

US-08-801-718-3
 ; Sequence 3, Application US/08801718
 ; Patent No. 5858976
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.

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; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,159A
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,515
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMBE UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-718-3

Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 125

RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; HILL, DAVID E.
; KINZLER, KENNETH W.
; VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/170,159A
; APPLICATION NUMBER: US/09/170,159A
; FILING DATE: 13-Oct-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.

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; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMBE UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

Query Match 98.9%; Score 548; DB 3; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 109
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RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
; APPLICANT: Sherri, Charles J
; APPLICANT: Quella, Dawn E
; APPLICANT: Weber, Jason D.
; APPLICANT: Rousel, Martine F.
; APPLICANT: Frederique, Zindy
; TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
; FILE REFERENCE: 1340-1-023 CIP 1
; CURRENT APPLICATION NUMBER: US/09/480,718
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 09/129,855
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-480-718-44

Query Match 98.9%; Score 548; DB 4; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSTSVSEN 125

RESULT 15
US-09-949-016-7125
; Sequence 7125, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7125
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7125

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Best Local Similarity 99.1%; Pred.No. 2.1e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      54  SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 113

QY      61  CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 109
Db     114  CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 162
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Job time : 45 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:24:54 ; Search time 697 Seconds
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51.098 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLVVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

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Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	98.9	491	9	US-09-888-077-1
2	548	98.9	491	9	US-09-956-425-8
3	548	98.9	491	10	US-09-029-327-2
4	548	98.9	491	11	US-09-966-724-2
5	548	98.9	491	15	US-10-422-536-137
6	548	98.9	491	15	US-10-232-951-35
7	548	98.9	491	16	US-10-685-838-1
8	531.5	95.9	216	13	US-10-057-510-4
9	522.5	94.3	522	15	US-10-287-226-380
10	522.5	94.3	522	15	US-10-287-226-382
11	488.5	88.2	489	9	US-09-956-425-6
12	488.5	88.2	489	11	US-09-966-724-4
13	481	86.8	95	16	US-10-685-838-2

14	472	85.2	95	16	US-10-685-838-4	Sequence 4, Appli
15	468	84.5	92	16	US-10-685-838-3	Sequence 3, Appli
16	309	55.8	59	14	US-10-211-088-143	Sequence 143, App
17	74.5	13.4	578	16	US-10-437-963-174237	Sequence 174237,
18	73.5	13.3	467	15	US-10-362-774-3	Sequence 3, Appli
19	73.5	13.3	467	15	US-10-369-493-6071	Sequence 6071, Ap
20	73	13.2	613	16	US-10-437-963-113326	Sequence 113326,
21	72	13.0	967	15	US-10-282-122A-59020	Sequence 59020, A
22	71	12.8	472	15	US-10-369-493-16585	Sequence 16585, A
23	71	12.8	473	15	US-10-282-122A-45311	Sequence 45311, A
24	70.5	12.7	79	15	US-10-424-599-236213	Sequence 236213,
25	70.5	12.7	350	10	US-09-746-783-54	Sequence 54, Appl
26	70.5	12.7	709	15	US-10-282-122A-63455	Sequence 63455, A
27	70.5	12.7	837	16	US-10-408-765A-2452	Sequence 2452, Ap
28	70	12.6	969	15	US-10-335-977-7409	Sequence 7409, Ap
29	70	12.6	972	15	US-10-335-977-7410	Sequence 7410, Ap
30	68	12.3	438	14	US-10-176-584A-2	Sequence 2, Appli
31	67.5	12.2	434	15	US-10-424-599-257589	Sequence 257589,
32	67.5	12.2	438	10	US-09-769-787-48	Sequence 48, Appl
33	67	12.1	368	15	US-10-389-566-382	Sequence 382, App
34	67	12.1	3092	9	US-09-801-368-172	Sequence 172, App
35	67	12.1	3092	15	US-10-369-493-1470	Sequence 1470, Ap
36	66.5	12.0	225	15	US-10-282-122A-52429	Sequence 52429, A
37	66.5	12.0	277	15	US-10-282-122A-75363	Sequence 75363, A
38	66.5	12.0	291	15	US-10-425-114-59572	Sequence 59572, A
39	66.5	12.0	372	16	US-10-437-963-169953	Sequence 169953,
40	66.5	12.0	422	15	US-10-369-493-7027	Sequence 7027, Ap
41	66.5	12.0	816	15	US-10-282-122A-61368	Sequence 61368, A
42	66	11.9	185	15	US-10-389-566-818	Sequence 818, App
43	66	11.9	320	16	US-10-437-963-133574	Sequence 133574,
44	66	11.9	418	15	US-10-389-566-819	Sequence 819, App
45	66	11.9	432	15	US-10-389-566-2420	Sequence 2420, App

ALIGNMENTS

RESULT 1
US-09-888-077-1
; Sequence 1, Application US/09888077
; Patent No. US20020031818A1
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; APPLICANT: Fuchs, Serge
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/IH195-US1
; CURRENT APPLICATION NUMBER: US/09/888,077
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-077-1

Query Match 98.9%; Score 548; DB 9; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKQTYTWKVELFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKQTYTWKVELFYLGQYIMTKRLYDEKQOHIVY 76
QY 61 CSNDLLGLFGVPFSVKEHKIYTMIVRNLYVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGLFGVPFSVKEHKIYTMIVRNLYVNVNQESSDSGTSVSEN 125

RESULT 2
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-425-8

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Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFVKHKKIYTMIRNLVVNQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSFVKHKKIYTMIRNLVVNQSSDSGTSVSEN 125

RESULT 3
US-09-956-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASIYLYK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-029-327-2

Query Match          98.9%; Score 548; DB 10; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 77 CSNDLLGDLFGVPSFVKHKKIYTMIRNLVVNQSSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELETYPE: 197430 BBME UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

Query Match          98.9%; Score 548; DB 11; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
 ; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
 ; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2
 ; OTHER INFORMATION: Mdm2 cDNA
 US-10-232-951-35

	Query Match	98.98;	Score 548;	DB 15;	Length 491;
	Best Local Similarity	99.11;	Pred. No. 2.8e-56;		
	Matches 108;	Conservative 1;	Mismatches 0;	Indels 0;	
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Qy	61	CSNDLLGDLPGVPFSFKVKEHKIYTMILRYNLVVVNNQOESSDSGTSVSSEN	109		
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Query Match	98.9%	Score 548;	DB 16;	Length 491;
Best Local Similarity	99.1%;	Pred. No. 2.8e-56;		
Matches 108;	Conservative	1;	Mismatches 0;	Indels 0;
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RESULT 8
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/10/057,510
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: USSN 09/510,252
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23

; PRIOR APPLICATION NUMBER: USN 60/122,643
 ; PRIOR FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
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 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-057-510-4

Query Match 95.9%; Score 531.5; DB 13; Length 216;
 Best Local Similarity 98.2%; Pred. No. 8.7e-55;
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Qy 61 CSDLLGLDGLFGVPSFVSKHRKIYTMVYRNLVVNVNQESSDSGTSVSEN 109

Db 76 CSDLLGLDGLFGVPSFVSKHRKIYTMVYRNLVVNVNQESSDSGTSVSEN 124

RESULT 9

US-10-287-226-380
 ; Sequence 380, Application US/10287226
 ; Publication No. US20040086875A1

GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,
 ; APPLICANT: Alsobrook, John P.,
 ; APPLICANT: Berghs, Constance,
 ; APPLICANT: Boldog, Ference,
 ; APPLICANT: Burgess, Catherine E.,
 ; APPLICANT: Chant, John S.,
 ; APPLICANT: Chaudhuri, Amitabha,
 ; APPLICANT: DiPippo, Vincent A.,
 ; APPLICANT: Edinger, Shlomit R.,
 ; APPLICANT: Eisen, Andrew,
 ; APPLICANT: Ellerman, Karen,
 ; APPLICANT: Gangolli, Esha A.,
 ; APPLICANT: Gorman, Linda,
 ; APPLICANT: Gerlach, Valerie,
 ; APPLICANT: Ji, Weizhen,
 ; APPLICANT: Kekuda, Ramesh,
 ; APPLICANT: Khrantsov, Nikolai,
 ; APPLICANT: Li, Li,
 ; APPLICANT: Malyankar, Uriel M.,
 ; APPLICANT: MacDougall, John R.,
 ; APPLICANT: Mezes, Peter S.,
 ; APPLICANT: Miller, Charles E.,
 ; APPLICANT: Millet, Isabelle,
 ; APPLICANT: Ooi, Chean Eng,
 ; APPLICANT: Ort, Tatiana,
 ; APPLICANT: Padigaru, Muralidhara,
 ; APPLICANT: Pattarajan, Meera,
 ; APPLICANT: Rastelli, Luca,
 ; APPLICANT: Rieger, Daniel K.,
 ; APPLICANT: Rothenberg, Mark E.,
 ; APPLICANT: Shenoy, Suresh G.,
 ; APPLICANT: Spaderna, Steven K.,
 ; APPLICANT: Spytek, Kimberley A.,
 ; APPLICANT: Taupier, Jr., Raymond J.,
 ; APPLICANT: Vernet, Corine A.M.,
 ; APPLICANT: Zerhusen, Bryan D.,
 ; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-480C
 ; CURRENT APPLICATION NUMBER: US/10/287,226
 ; CURRENT FILING DATE: 2002-11-04
 ; PRIOR APPLICATION NUMBER: 60/334,421
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/354,392
 ; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: 60/360,148
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: 60/364,000
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 60/404,821
 ; PRIOR FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 60/334,526
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/354,409
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 60/364,227
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 60/334,027
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: 60/331,641
 ; PRIOR FILING DATE: 2001-11-20
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 673
 ; SOFTWARE: Curaseqlist version 0.1
 ; SEQ ID NO 380
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-287-226-380

Query Match 94.3%; Score 522.5; DB 15; Length 522;

Best Local Similarity 77.1%; Pred. No. 3.3e-53;

Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDYTTMKVEVLYLGQYIMTKRLYDEKQOHVH 36

Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDYTTMKRWSFTMLPRLVNVNSWAQICLPRP 76

Qy 37 -----VLFYLGQYIMTKRLYDEKQOHVHCNSDGLDGLFGVPSFVSKHRKIYTMVYR 89

Db 77 PKVLDLQVLFYLGQYIMTKRLYDEKQOHVHCNSDGLDGLFGVPSFVSKHRKIYTMVYR 136

Qy 90 NLVVNVNQESSDSGTSVSEN 109

Db 137 NLVVNVNQESSDSGTSVSEN 156

RESULT 10

US-10-287-226-382
 ; Sequence 382, Application US/10287226
 ; Publication No. US20040086875A1

GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,
 ; APPLICANT: Alsobrook, John P.,
 ; APPLICANT: Berghs, Constance,
 ; APPLICANT: Boldog, Ference,
 ; APPLICANT: Burgess, Catherine E.,
 ; APPLICANT: Chant, John S.,
 ; APPLICANT: Chaudhuri, Amitabha,
 ; APPLICANT: DiPippo, Vincent A.,
 ; APPLICANT: Edinger, Shlomit R.,
 ; APPLICANT: Eisen, Andrew,
 ; APPLICANT: Ellerman, Karen,
 ; APPLICANT: Gangolli, Esha A.,
 ; APPLICANT: Gorman, Linda,
 ; APPLICANT: Gerlach, Valerie,
 ; APPLICANT: Ji, Weizhen,
 ; APPLICANT: Kekuda, Ramesh,
 ; APPLICANT: Khrantsov, Nikolai,
 ; APPLICANT: Li, Li,
 ; APPLICANT: Malyankar, Uriel M.,
 ; APPLICANT: MacDougall, John R.,
 ; APPLICANT: Mezes, Peter S.,
 ; APPLICANT: Millet, Charles E.,
 ; APPLICANT: Millet, Isabelle,
 ; APPLICANT: Ooi, Chean Eng,
 ; APPLICANT: Ort, Tatiana,
 ; APPLICANT: Padigaru, Muralidhara,


```
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spadeina, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-382

Query Match 94.3%; Score 522.5; DB 15; Length 522;
Best Local Similarity 77.1%; Pred. No. 3.3e-53;
Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE----- 36
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERSFTMLPRLVWNSWAQIGICLRP 76
Qy 37 -----VLFYLGQYIMTKRLYDEKQOHVHCNSDLLGDLFGVPSFSVKEHRKIYTMLYR 89
Db 77 PKVLDQLVLFYLGQYIMTKRLYDEKQOHVHCNSDLLGDLFGVPSFSVKEHRKIYTMLYR 136
Qy 90 NLVVVNQSSDSGTSVSEN 109
Db 137 NLVVVNQSSDSGTSVSEN 156

RESULT 11
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
```

```
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-956-425-6

Query Match 88.2%; Score 488.5; DB 9; Length 489;
Best Local Similarity 87.2%; Pred. No. 3.3e-49;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTMKEIIFYIGQYIMTKRLYDEKQOHIV 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQSSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYMIYRNILVAVSQO---DSGTSLSSES 122

RESULT 12
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

Query Match 88.2%; Score 488.5; DB 11; Length 489;
Best Local Similarity 87.2%; Pred. No. 3.3e-49;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;
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Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTMKEIIFYIGQYIMTKRLYDEKQOQHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDGTSTVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVANVAVSQ---DSGTSLSSES 122

RESULT 13
US-10-685-838-2
; Sequence 2, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
; APPLICANT: SHUBERT, CARSTEN
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-685-838-2

Query Match 86.8%; Score 481; DB 16; Length 95;
Best Local Similarity 98.9%; Pred. No. 3e-49;
Matches 94; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVH 60
Db 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVY 60
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVN 95
Db 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVN 95

RESULT 14
US-10-685-838-4
; Sequence 4, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
; APPLICANT: SHUBERT, CARSTEN
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-685-838-4

Query Match 85.2%; Score 472; DB 16; Length 95;
Best Local Similarity 97.9%; Pred. No. 3.5e-48;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVH 60
Db 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVY 60
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVN 95
Db 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVN 95

RESULT 15
US-10-685-838-3
; Sequence 3, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
; APPLICANT: SHUBERT, CARSTEN
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-685-838-3

Query Match 84.5%; Score 468; DB 16; Length 92;
Best Local Similarity 98.9%; Pred. No. 1e-47;
Matches 91; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLL 66
Db 1 EQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVCSNDLL 60
Qy 67 GDLFGVPSFSVKEHRKIYTMIRNLVVVNQOE 98
Db 61 GDLFGVPSFSVKEHRKIYTMIRNLVVVNQOE 92

Search completed: February 16, 2005, 08:50:04
Job time : 698 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 38 Seconds
(without alignments)
275.990 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	98.9	491	1 S24354	p53-binding protei
2	488.5	88.2	489	2 S15349	mdm2 protein - mco
3	271.5	49.0	489	2 S71955	MDM2-like p53-bind
4	84	15.2	685	1 SXBPT4	NAD+-protein ADP-r
5	84	15.2	698	1 S31630	NAD+-protein ADP-r
6	84	15.2	698	1 S31714	NAD+-protein ADP-r
7	73.5	13.3	467	2 T25848	hypothetical prote
8	72.5	13.1	565	2 S52682	hypothetical prote
9	72.5	13.1	2833	2 A43360	inositol 1,4,5-tri
10	72	13.0	967	2 A64710	type III restricti
11	71.5	12.9	514	2 D85069	hypothetical prote
12	70.5	12.7	709	2 E64213	DNA topoisomerase
13	70.5	12.7	838	2 I45557	eyeless, long form
14	70	12.6	969	2 E71810	type III restricti
15	68	12.3	134	2 G69382	response regulator
16	67	12.1	176	2 JQ1813	B19R protein - vac
17	67	12.1	181	2 S75415	probable ribosomal
18	67	12.1	261	2 H71680	exodeoxyribonuclea
19	67	12.1	3092	2 A60009	GTPase-activating
20	66.5	12.0	422	2 T26334	hypothetical prote
21	66.5	12.0	447	2 I64002	sodium-translocat
22	66.5	12.0	517	2 S32169	hypothetical prote
23	65.5	11.8	277	2 A10589	conserved hypothet
24	65.5	11.8	339	2 A90395	conserved hypothet
25	65.5	11.8	425	2 T50184	mammalian swi/snf
26	65.5	11.8	450	2 G70210	conserved hypot
27	65.5	11.8	704	2 H82381	toxin secretion AT
28	65	11.7	232	2 E82501	hypothetical prote
29	65	11.7	260	2 T28182	hypothetical prote

30	64.5	11.6	331	2 B84938	flagellar motor sw
31	64.5	11.6	525	2 T15185	hypothetical proce
32	64	11.6	286	2 B97743	exodeoxyribonuclea
33	64	11.6	316	2 F69491	methenyltetrahydro
34	64	11.6	346	2 G72094	ct244 hypothetical
35	64	11.6	346	2 G86528	CT244 hypothetical
36	64	11.6	346	2 B81574	conserved hypothet
37	64	11.6	369	2 B70220	conserved hypothet
38	64	11.6	488	2 T47943	1-aminocyclopropan
39	64	11.6	600	2 H81733	DNA primase TC0175
40	64	11.6	855	2 B89472	protein ZCS3.4 (im
41	64	11.6	860	2 S64366	hypothetical prote
42	64	11.6	908	2 C70168	DNA polymerase I (
43	64	11.6	1026	2 C71490	probable exodeoxyr
44	63.5	11.5	353	2 D69001	conserved hypothet
45	63.5	11.5	366	2 T07827	1-aminocyclopropan

ALIGNMENTS

RESULT 1

S24354

p53-binding protein mdm2 - human

N:Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phosph

N:Contains: p53-binding protein mdm2, splice form A

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: S24354; S57338; G02026

R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.

Nature 358, 80-83, 1992

A:Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.

A:Reference number: S24354; MUID:92310576; PMID:1614537

A:Accession: S24354

A:Molecule type: mRNA

A:Residues: 1-491 <OLI>

A:Cross-references: EMBL:Z12020; NID:G35211; PIDN:CAA78055.1; PID:G35212

R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.

Nucleic Acids Res. 23, 2584-2592, 1995

A:Title: A functional p53-responsive intronic promoter is contained within the human mdm

A:Reference number: S57338; MUID:95380270; PMID:7651818

A:Accession: S57338

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-16,'P',18-24 <ZAU>

A:Cross-references: EMBL:U28935; NID:G904033; PIDN:AAA82237.1; PID:G904034

R:Lunec, J.

submitted to the EMBL Data Library, August 1995

A>Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding dom

A:Reference number: G09070

A:Accession: G02026

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-27,223-491 <LUN>

A:Cross-references: EMBL:U33199; NID:G992676; PIDN:AAA75514.1; PID:G992677

A:Experimental source: splice form A

C:Genetics:

A:Gene: GDB:MDM2

A:Cross-references: GDB:250456; OMIM:164785

A:Map position: 12q14.3-12q15

C:Superfamily: human p53-binding protein mdm2

C:Keywords: alternative splicing; oncogene; phosphoprotein

F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT>

F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT>

Query Match 98.9%; Score 548; DB 1; Length 491;

Best Local Similarity 99.1%; Pred. No. 5e-49; Indels 0; Gaps 0;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLSVGAQDITYTMKEVLFYLGQYIMTKRLYDEKQOHVH 60

|||||

Db 17 SQIPASEQETLVRPKPLLLKLSVGAQDITYTMKEVLFYLGQYIMTKRLYDEKQOHVY 76

|||||

QY 61 CSNDLLGDLFGVPSFVSKHRKIYTMIRNVLVNVNQESSDSGTSVSEN 109
|||||
Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIRNVLVNVNQESSDSGTSVSEN 125
|||||

RESULT 2

S15349
mdm2 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S15349
R: Pakharzadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1563-1569, 1991
A:Title: Tumorigenic potential associated with enhanced expression of a gene that is amplified in human p53-binding protein mdm2
A:Reference number: S15349; MUID:91224107; PMID:2026149
A:Accession: S15349
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-489 <PAK>
A:Cross-references: UNIPROT:P23804; EMBL:X58876; NID:G53038; PIDN:CAA41684.1; PID:G53039
C:Genetics:
A:Gene: mdm2
C:Superfamily: human p53-binding protein mdm2

Query Match 88.2%; Score 488.5; DB 2; Length 489;
Best Local Similarity 87.2%; Pred. No. 7.4e-43;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

QY 1 SQIPASEQETLVRPRLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHLVH 60
|||||
Db 17 SQIPASEQETLVRPRLLLKLLKSVGAQNDTYTMKEIFYIGQYIMTKRLYDEKQOHIVY 76
|||||

QY 61 CSNDLLGDLFGVPSFVSKHRKIYTMIRNVLVNVNQESSDSGTSVSEN 109
|||||
Db 77 CSNDLLGDLFGVPSFVSKHRKIYTMIRNVLVNVNQESSDSGTSLSSES 122
|||||

RESULT 3

S71955
MDM2-like p53-binding protein MDMX - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S71955
R: Shwarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van Hattum, J. 15, 5349-5357, 1996
A:Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A:Reference number: S71955; MUID:97050840; PMID:8895579
A:Accession: S71955
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-489 <SHV>
A:Cross-references: UNIPROT:Q35618; EMBL:AF007110; NID:G2253388; PIDN:AAB62927.1; PID:G2253389
C:Genetics:
A:Gene: MDMX
C:Function:
A:Description: inhibits transcription activation function of tumour suppressor protein p53
C:Superfamily: human p53-binding protein mdm2

Query Match 49.0%; Score 271.5; DB 2; Length 489;
Best Local Similarity 52.4%; Pred. No. 2.4e-20;
Matches 55; Conservative 17; Mismatches 22; Indels 11; Gaps 1;

QY 5 ASEQETLVRPRLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHLVHCSND 64
:|||||
Db 20 SSEQISQVRPKLQLLLKILHAAGAQQEVFTMKVVMHLYGQYIMVKQLYDQOQHVMVYCGD 79
:|||||

QY 65 LLGDLFGVPSFVSKHRKIYTMIRNVLVNVNQESSDSGTSVSEN 109
|||||
Db 80 LLGDLFGVPSFVSKDPSFLYDMLRKNLV-----TSASNN 113
|||||

RESULT 4

SXBPT4

NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T4
C:Species: phase T4
A:Note: host Escherichia coli
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: J00096
R: Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A:Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A:Reference number: J00096; MUID:89386005; PMID:2506526
A:Accession: J00096
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-685 <HIL>
A:Cross-references: UNIPROT:P12726
C:Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits of F1-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>
C:Genetics:
A:Gene: alt
C:Superfamily: phase T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase
F:7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

Query Match 15.2%; Score 84; DB 1; Length 685;
Best Local Similarity 29.0%; Pred. No. 0.98;
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

QY 18 LLKLLKS--VGAQKDTYTMKEVLFY---GOYIMTKRL--YDEKQOHI-VHCSNDLLGDL 69
:|||||
Db 111 MLRLKSKTAGAQRQIQVIADRLRSRGGRYLLKELWDYDKYAVILIRKNVSLDI 170
:|||||

QY 70 FGVPFSFVSKHRKIYTMIRNVLVNVNQESSDSGTSVSEN 109
|||||
Db 171 FGVPFISTELFTKVESKV--GDVYINK---DTGAQVTKN 204
|||||

RESULT 5

S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T2
C:Species: phase T2
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31630
R: Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A:Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A:Reference number: S31630
A:Accession: S31630
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <KOC>
A:Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:G15187; PIDN:CAA49517.1; PID:G15188
C:Superfamily: phase T4 NAD-protein ADP-ribosyltransferase
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 15.2%; Score 84; DB 1; Length 698;
Best Local Similarity 29.0%; Pred. No. 1;
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

QY 18 LLKLLKS--VGAQKDTYTMKEVLFY---GOYIMTKRL--YDEKQOHI-VHCSNDLLGDL 69
:|||||
Db 112 MLRLKSKTAGAQRQIQVIADRLRSRGGRYLLKELWDYDKYAVILIRKNVSLDI 171
:|||||

QY 70 FGVPFSFVSKHRKIYTMIRNVLVNVNQESSDSGTSVSEN 109
|||||
Db 172 FGVPFISTELFTKVESKV--GDVYINK---DTGAQVTKN 205
|||||

RESULT 6

S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phase T6
C:Species: phase T6
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S31714
R: Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992

A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6; Sequencing of
A;Reference number: S31630
A;Accession: S31714
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 15.2%; Score 84; DB 1; Length 698;
Best Local Similarity 29.0%; Pred. No. 1;
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

Qy 18 LKLKLS--VGAQKDYYTWKEVLFFYL---QQYIMTKRL--YDEKQOHI-VHCSNDLLIGDL 69
Db 112 MLAILSKTAGAQIQVIADRILRSRSGRYLLKELWDYDKYAYILHRKNVSLEDI 171
Qy 70 FGVPSPVKGHRKIYTIWYNLVNVNQSSDSGTSVSEN 109
Db 172 PGVPEISTELTFVESKV--GDVVINK---DTGAQVTKN 205

RESULT 7
T25848
hypothetical protein T01B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25848
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
A;Accession: T25848
A;Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A;Residues: 1-467 <GEI>
A;Cross-references: UNIPROT:P91408; EMBL:U80931; PIDN:AAB37999.1; GSPDB:GN00022; CESP:T01B11
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
A;Gene: CESP:T01B11.2
A;Map position: 4
A;Introns: 39/2; 79/1; 131/2; 156/2; 337/3; 389/2
C;Superfamily: ornithine-oxo-acid aminotransferase

Query Match 13.3%; Score 73.5; DB 2; Length 467;
Best Local Similarity 32.9%; Pred. No. 7.7;
Matches 25; Conservative 5; Mismatches 25; Indels 21; Gaps 3;

Qy 1 SQTPASQEETLVRPKPLLKLSVGAKDYYTMKEVLFFYLGGQYIMTKR-----LYDEKQ 55
Db 13 SSTFPAATXDVRSKEILK-----RRKTIGSKCOIFYSDDPPFWVRASMQLYDEKS 66
Qy 56 -----OHIVHC 61
Db 67 NKFLDCISNVQHVGHC 82

RESULT 8
S52682
hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.12c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52682
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52671
A;Accession: S52682
A:Molecule type: DNA
A;Residues: 1-565 <MUR>
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:G747879; PID:G747891; GSPDB:GN00004
C;Genetics:

Query Match 13.0%; Score 72; DB 2; Length 967;
Best Local Similarity 24.8%; Pred. No. 26;
Matches 26; Conservative 21; Mismatches 44; Indels 14; Gaps 3;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKR---LYDEKQOH 57
DB 768 NEIKNEQEGRLLELEFLIYIYQNIKDISYQMRRTI-----IKNKDAFYDEKGEI 821

QY 58 IVHCSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDS 102
DB 822 REFLLDGLGADKYEIKNSVRE-----KCLYENFMQVDSEIEKDT 861

RESULT 11
D85069
hypothetical protein AT4G05520 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85069
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85069
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-514 <STO>
A:Cross-references: UNIPROT:Q9S9W1; GB:NC_001268; NID:G7267312; PIDN:CAB81094.1; GSPDB:C
C:Genetics:
A:Gene: AT4G05520
A:Map position: 4

Query Match 12.9%; Score 71.5; DB 2; Length 514;
Best Local Similarity 29.7%; Pred. No. 14;
Matches 27; Conservative 13; Mismatches 26; Indels 25; Gaps 4;

QY 15 KPILLKLLKSVGA-----QKDTYTMKEVLFYLGQY-----IMTKRLYDEKQOH 58
DB 384 QPLFLKLMRYGALMWSLGLKVLNTPVVRVYIGSFNDKPFINEVAVGPICKELFEKEQ--- 440

QY 59 VHCNSNDLLGDLFGVPSFSVKEHRKIYTMIR 89
DB 441 ----NDLLADLMDVPKKAC--DRKINEFVKR 465

RESULT 12
E64213
DNA topoisomerase (EC 5.99.1.2) - Mycoplasma genitalium
N:Alternate names: type I DNA topoisomerase
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: E64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: E64213
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-709 <TIGR>
A:Cross-references: UNIPROT:P47368; GB:U39691; GB:L43967; NID:G1045794; PID:G1045802; TI
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: DNA topoisomerase I
C:Keywords: isomerase

Query Match 12.7%; Score 70.5; DB 2; Length 709;
Best Local Similarity 23.4%; Pred. No. 26;
Matches 22; Conservative 18; Mismatches 45; Indels 9; Gaps 2;

QY 21 LLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDE-----KQOHVHCNSNDLLGDLFGVPSF 75
DB 431 IVFINKNKFTYSSKSLFDGY---QRLYEIKNTKDELIDYIDLSKLKIGKPFSEKI 486

QY 76 SVKEHRKIYTMIRNLVVNQESSDSCTSUSEN 109
DB 487 SVNEHKTNPFPYTOASLIEELEKSNIGRPSTYN 520

RESULT 13
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C:Accession: I45557
R:Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science 265, 785-789, 1994
A:Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A:Reference number: A54584; MUID:94323757; PMID:7914031
A:Accession: I45557
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-838 <RES>
A:Cross-references: EMBL:X79493; NID:G641809; PIDN:CAA56038.1; PID:G641810
C:Genetics:
A:Gene: FlyBase:ey
A:Cross-references: FlyBase:FBgn0005558
A:Introns: 37/1; 92/3; 152/3; 371/1; 429/1; 521/1; 639/2
C:Superfamily: homeobox homology; paired box homology
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulatu
F:37-161/Domain: paired box homology <PBH>
F:412-468/Domain: homeobox homology <HOX>

Query Match 12.7%; Score 70.5; DB 2; Length 838;
Best Local Similarity 26.0%; Pred. No. 31;
Matches 26; Conservative 14; Mismatches 33; Indels 27; Gaps 5;

QY 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQY-----IMTKRLYDEKQOHVHCNSDL 65
DB 99 IRP-----RAITGSKPRVATAEVVSKISQYKRCPSFAWEIRDRLIQENV-CTND- 148

QY 66 LGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTS 105
DB 149 ----NIPSVS-----SINRVLRLAAQKEQQSTGSGSS 177

RESULT 14
E71810
type III restriction enzyme - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71810
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-969 <ARN>
A:Cross-references: UNIPROT:Q9ZJ3; GB:AE001563; GB:AE001439; NID:G4156027; PIDN:RAD0698
A:Experimental source: strain J99
C:Genetics:
A:Gene: res_2

Query Match 12.6%; Score 70; DB 2; Length 969;
Best Local Similarity 22.9%; Pred. No. 41;
Matches 24; Conservative 20; Mismatches 47; Indels 14; Gaps 3;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKR---LYDEKQOH 57
DB 768 NEIKNEQEGRLLELEFLIYIYQNIKDISYQMRRTI-----IKNKDAFYDEKGEI 821

Db 770 NEIKKNEQGLKRLLEFLLEIIYQNIKOKISYQMBETT-----IKNRKNDAFYDEKGE- 822

QY 58 IVHCNSNDLLGLDLFGVPSFSVKEHRKIYTIYTNLVVNOQESSDS 102

Db 823 ----IREFLDGSLGADKYEIKNSSAQEKCLYENFMQVDSEIEKDT 863

RESULT 15

G69382

response regulator homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: G69382

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: G69382

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-134 <KLE>

A:Cross-references: UNIPROT:Q29199; GB:AE001029; GB:AE000782; NID:92589352; PIDN:AB9017

C:Superfamily: signal transduction receiver (phosphoacceptor) protein, Chey type; respon

C:Keywords: phosphoprotein

F:20-126/Domain: response regulator homology <RRH>

P:66/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 12.3%; Score 68; DB 2; Length 134;

Best Local Similarity 28.4%; Pred. No. 6.8;

Matches 21; Conservative 15; Mismatches 38; Indels 0; Gaps 0;

QY 35 KEVLFLVGYIMTKRLYDEKQKHVHCNSNDLLGLDLFGVPSFSVKEHRKIYTIYTNLVV 94

Db 6 KFLFWLHPNIMTKILVDDDCSICELYKILGSFEVWSACSGREGLELYRKIMPDLVIV 65

QY 95 NQESSSDSGTSVSE 108

Db 66 DINMPDISGVEVAK 79

Search completed: February 16, 2005, 08:24:51

Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 170 Seconds
(without alignments)
328.333 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLVVRPKPLLLK.....NLVVNQSSDSTGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	548	98.9	166	Q8NDW2	Q8ndw2 homo sapien
2	548	98.9	195	Q96DS4	Q96ds4 homo sapien
3	548	98.9	243	Q8TE47	Q8te47 homo sapien
4	548	98.9	491	1 MDM2_HUMAN	Q00987 homo sapien
5	536	96.8	487	1 MDM2_CANPA	P56950 canis famil
6	536	96.8	487	2 Q9GMZ6	Q9gmz6 canis famil
7	536	96.8	491	1 MDM2_HORSE	P56951 equus cabal
8	533	96.2	491	2 Q7YRZ8	Q7yrz8 felis silve
9	498	88.2	436	2 Q8WYJ2	Q8wyj2 homo sapien
10	488.5	88.2	489	1 MDM2_MOUSE	P23804 mus musculus
11	488.5	88.2	489	2 Q91XK7	Q91xk7 m mus muscu
12	471	85.0	118	2 Q8WYJ3	Q8wyj3 homo sapien
13	464.5	83.8	466	1 MDM2_MESAU	Q60524 mesocricetu
14	421	76.0	325	2 Q8TE46	Q8te46 homo sapien
15	402	72.6	173	2 Q8TE46	Q8te46 homo sapien
16	364	65.7	473	1 MDM2_XENLA	P56273 xenopus lae
17	364	65.7	473	2 Q6GMB5	Q6gmb5 xenopus lae
18	363	65.5	482	2 Q6P3O9	Q6p3q9 xenopus tro
19	334	60.3	105	2 Q8NDW0	Q8ndw0 homo sapien
20	315	56.9	426	2 Q9GK41	Q9gk41 canis famil
21	298.5	53.9	445	1 MDM2_BRARE	Q42354 brachydanielo
22	280.5	50.6	446	2 Q8WYJ1	Q8wyj1 homo sapien
23	274	49.5	491	2 Q7ZUW7	Q7zuw7 brachydanielo
24	272	49.1	475	2 Q7ZYI3	Q7zyi3 xenopus lae
25	271.5	49.0	489	1 MDM4_MOUSE	Q35618 mus musculus
26	268.5	48.5	489	2 Q9CYG1	Q9cyg1 m mus muscu
27	262	47.3	490	2 Q99L86	Q99l86 mus musculus
28	260.5	47.0	134	2 Q6PHL8	Q6phl8 xenopus lae
29	246	44.4	140	2 Q68DC0	Q68dc0 homo sapien
30	246	44.4	153	2 Q6MZR7	Q6mzr7 homo sapien
31	244	44.0	490	1 MDM4_HUMAN	O15151 homo sapien

32	223	40.3	69	2	Q86WA4	Q86wa4 homo sapien
33	216	39.0	66	2	Q86DS3	Q86ds3 homo sapien
34	213	38.4	70	2	Q86WA3	Q86wa3 homo sapien
35	199	35.9	95	2	Q96DS1	Q96ds1 homo sapien
36	179.5	32.4	70	2	Q8NDW1	Q8ndw1 homo sapien
37	177	31.9	159	2	Q96DS0	Q96ds0 homo sapien
38	176	31.8	60	2	Q96DS5	Q96ds5 homo sapien
39	176	31.8	130	2	Q9H4C3	Q9h4c3 homo sapien
40	176	31.8	243	2	Q9H4C5	Q9h4c5 homo sapien
41	175	31.6	65	2	Q86WA5	Q86wa5 homo sapien
42	156	28.2	50	2	Q8NDV9	Q8ndv9 homo sapien
43	119.5	21.6	54	2	Q86WA2	Q86wa2 homo sapien
44	84.5	15.3	1132	2	O40913	O40913 human herpe
45	84	15.2	682	1	ALT_BPT4	P12726 bacterioph

ALIGNMENTS

RESULT 1

Q8NDW2 PRELIMINARY; PRT; 166 AA.
 AC Q8NDW2;
 DT 01-OCT-2002 (TremBLrel. 22, Created)
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE P53-binding protein.
 GN Name=MDM2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartel F., Pinkert D., Kappeler M., Bache M., Schmidt H., Taubert H.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ491698; CAD36959.1; -;
 DR HSSP; Q9UMT8; IYCR.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR InterPro; IPR010984; MDM2.
 DR InterPro; IPR003121; SWIB_MDM2.
 DR Pfam; PF02201; SWIB; 1.
 SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 98.9%; Score 548; DB 2; Length 166;
 Best Local Similarity 99.1%; Pred. No. 7.1e-51;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVVRPKPLLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

Db 17 SQIPASEQETLVVRPKPLLLKLSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIVRNLVNQQSSDSTGTSVSEN 109

Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIVRNLVNQQSSDSTGTSVSEN 125

RESULT 2

Q96DS4 PRELIMINARY; PRT; 195 AA.
 AC Q96DS4;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE MDM2 variant FB26.
 GN Name=MDM2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rhabdomyosarcoma tumor;

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF385323; AAL13243.1; -;
DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB_MDM2.

DR Pfam; PF02201; SWIB; 1.

SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12D5D CRC64;

Query Match 98.9%; Score 548; DB 2; Length 195;

Best Local Similarity 99.1%; Pred. No. 8.5e-51;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60

DB 17 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPFSVKEHRKIYTYMIRNLVNVNQESSDSGTSVSEN 109

DB 77 CSNDLLGLDGLFGVPFSVKEHRKIYTYMIRNLVNVNQESSDSGTSVSEN 125

RESULT 3

Q8TE47

ID Q8TE47 PRELIMINARY; PRT; 243 AA.

AC Q8TE47;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 isoform KB9 protein.

GN Name=MDM2 isoform KB9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphocytes;

RA Bartel F., Pinkert D., Kappeler M., Bache M., Schmidt H., Taubert H.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ30612; CND23251.1; -;

DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0001051; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0016567; F:protein ubiquitination; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB_MDM2.

DR Pfam; PF02201; SWIB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

SQ SEQUENCE 243 AA; 27317 MW; 9B5DD0142CF185A2 CRC64;

Query Match

Best Local Similarity 98.9%; Score 548; DB 2; Length 243;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60

DB 17 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPFSVKEHRKIYTYMIRNLVNVNQESSDSGTSVSEN 109

DB 77 CSNDLLGLDGLFGVPFSVKEHRKIYTYMIRNLVNVNQESSDSGTSVSEN 125

RESULT 4

MDM2_HUMAN

ID_MDM2_HUMAN STANDARD; PRT; 491 AA.

AC Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;

AC

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).

GN Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RX MEDLINE=92310576; PubMed=1614537; DOI=10.1038/358080a0;

RA Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;

RT "Amplification of a gene encoding a p53-associated protein in human sarcomas.";

RL Nature 358:80-83 (1992).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).

RC TISSUE=Ovarian carcinoma;

RX MEDLINE=963113107; PubMed=8705862;

RA Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;

RT "Alternatively spliced mdm2 transcripts with loss of p53 binding domain sequences: transforming ability and frequent detection in human cancer.";

RL Nat. Med. 2:912-917 (1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).

RX MEDLINE=20065171; PubMed=10597303; DOI=10.1038/sj.onc.1203182;

RA Veidhoen N., Metcalfe S., Milner J.;

RT "A novel exon within the mdm2 gene modulates translation initiation in vitro and disrupts the p53-binding domain of mdm2 protein.";

RL Oncogene 18:7026-7033 (1999).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,

RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;

RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esg.gs.washington.edu).";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM MDM2).

RC TISSUE=Muscle;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [6]

RP SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).

RA Liang H., Atkins H., Abdel-Fattah R., Suaeun R., Lunec J.;

RT "Genomic organisation of the human MDM2 oncogene and relationship to its alternatively spliced mRNA's";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [7]

SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE=95380270; PubMed=7651818;
RA Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;
RT "A functional p53-responsive intronic promoter is contained within the
RL human mdm2 gene.";
RN Nucleic Acids Res. 23:2584-2592(1995).
RP
SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=97413643; PubMed=9270029;
RA Landers J.B., Cassel S.L., George D.L.;
RT "Translational enhancement of mdm2 oncogene expression in human tumor
RL cells containing a stabilized wild-type p53 protein.";
RN Cancer Res. 57:3562-3568(1997).
RP
SEQUENCE OF 301-481 FROM N.A.
RX MEDLINE=20542019; PubMed=11087894; DOI=10.1016/S0027-5107(00)00112-3;
RA Taubert H., Kappler M., Meyer A., Bartel F., Schlott T.,
RL Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;
RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in
RL normal blood donors and in soft tissue sarcoma patients: an indication
RL for an increased cancer susceptibility?";
RN Mutat. Res. 456:39-44(2000).
RP
MUTAGENESIS OF CYS-464.
RX MEDLINE=98111004; PubMed=9450543; DOI=10.1016/S0014-5793(97)01480-4;
RA Honda R., Tanaka H., Yasuda H.;
RL "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";
RN FEBS Lett. 420:25-27(1997).
RP
MUTAGENESIS OF CYS-449.
RX MEDLINE=20190101; PubMed=10723139; DOI=10.1038/sj.onc.1203464;
RA Honda R., Yasuda H.;
RL "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is
RL dependent on the RING finger domain of the ligase.";
RN Oncogene 19:1473-1476(2000).
RP
MUTAGENESIS.
RX MEDLINE=20187618; PubMed=10722742; DOI=10.1074/jbc.275.12.8945;
RA Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;
RL "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself
RL and p53.";
RN J. Biol. Chem. 275:8945-8951(2000).
RP
MUTAGENESIS OF CYS-441 AND CYS-478.
RX MEDLINE=20076498; PubMed=10608892; DOI=10.1074/jbc.274.53.38189;
RA Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;
RL "Stabilization of the MDM2 oncoprotein by interaction with the
RL structurally related DMX protein.";
RN J. Biol. Chem. 274:38189-38196(1999).
RP
NUCLEOLAR LOCALIZATION SIGNAL.
RX MEDLINE=20173879; PubMed=10707090; DOI=10.1038/35004057;
RA Lohrum M.A.E., Aehcroft M., Kubbutat M.H.G., Vousden K.H.;
RL "Identification of a cryptic nucleolar-localization signal in MDM2.";
RN Nat. Cell Biol. 2:179-181(2000).
RP
PHOSPHORYLATION BY ATM.
RX MEDLINE=20079591; PubMed=10611322; DOI=10.1073/pnas.96.26.14973;
RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RL "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RL in response to DNA damage.";
RN Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
RP
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.
RX MEDLINE=97081050; PubMed=8875929; DOI=10.1126/science.274.5289.948;
RA Kusie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
RL Levine A.J., Pavletich N.P.;
RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
RL transactivation domain.";
RN Science 274:948-953(1996).
CC
-!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC
apoptosis by binding its transcriptional activation domain.
CC

toward p53 and itself. Permits the nuclear export of p53 and
targets it for proteasome-mediated proteolysis.
CC
-!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC
-!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor.
CC
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm. Interaction with ARF(p14)
CC results in the localization of both proteins to the nucleolus. The
CC nucleolar localization signals in both ARF(p14) and MDM2 may be
CC necessary to allow efficient nucleolar localization of both
CC proteins.
CC
-!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=8;
CC Name=Mdm2;
CC IsoId=Q00987-1; Sequence=Displayed;
CC Name=Mdm2-A;
CC IsoId=Q00987-2; Sequence=VSP_003208;
CC Name=Mdm2-A1;
CC IsoId=Q00987-3; Sequence=VSP_003208, VSP_003214;
CC Name=Mdm2-B;
CC IsoId=Q00987-4; Sequence=VSP_003209;
CC Name=Mdm2-C;
CC IsoId=Q00987-5; Sequence=VSP_003211;
CC Name=Mdm2-D;
CC IsoId=Q00987-6; Sequence=VSP_003210;
CC Name=Mdm2-E;
CC IsoId=Q00987-7; Sequence=VSP_003212, VSP_003213;
CC Name=Mdm2-alpha;
CC IsoId=Q00987-8; Sequence=VSP_003207;
CC
-!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E
CC are observed in a range of human cancers but absent in normal
CC tissues.
CC
-!- INDUCTION: By DNA damage.
CC
-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC Region II contains most of a central acidic region required for
CC interaction with ribosomal protein L5 and a putative C4-type zinc
CC finger. The RING finger domain which coordinates two molecules of
CC zinc interacts specifically with RNA whether or not zinc is
CC present and mediates the hetero-oligomerization with MDM4. It is
CC also essential for its ubiquitin ligase E3 activity toward p53 and
CC itself.
CC
-!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC dependent manner.
CC
-!- DISEASE: Seems to be amplified in certain tumors (including soft
CC tissue sarcomas, osteosarcomas and gliomas). A higher frequency of
CC splice variants lacking p53 binding domain sequences was found in
CC late-stage and high-grade ovarian and bladder carcinomas. Four of
CC the splice variants show loss of p53 binding.
CC
-!- MISCELLANEOUS: MDM2 RING finger mutations that failed to
CC
Query Match 98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.4e-50;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDYTMKEVLFLYLGQYIMTKRLYDEKQOHVH 60
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDYTMKEVLFLYLGQYIMTKRLYDEKQOHVY 76
QY 61 CSNDLLGLDPLFGVPSFSVKEHRKIYTMVYRNVLVNVNQSSDSGTSVSEN 109
DB 77 CSNDLLGLDPLFGVPSFSVKEHRKIYTMVYRNVLVNVNQSSDSGTSVSEN 125

RESULT 5
MDM2 CANFA
ID MDM2 CANFA STANDARD; PRT; 487 AA.
AC P56950; Q95KNS;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
GN Name=MDM2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-484 FROM N.A.
RX MEDLINE=20219866; PubMed=10754200; DOI=10.1016/S0304-3835(99)00427-9;
RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA Argyle D.J.;
RT "Cloning, sequence analysis and expression of the cDNAs encoding the
RT canine and equine homologues of the mouse double minute 2 (mdm2)
RT proto-oncogene.";
RL Cancer Lett. 152:9-13 (2000).
[2]
RP SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).
RX MEDLINE=20065171; PubMed=10597303; DOI=10.1038/sj.onc.1203182;
RA Velthoen N., Metcalfe S., Milner J.;
RT "A novel exon within the mdm2 gene modulates translation initiation in
RT vitro and disrupts the p53-binding domain of mdm2 protein.";
RL Oncogene 18:7026-7033 (1999).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis (By similarity).
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC similarity).
CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB). E1A-associated protein EP300 and the E2F1 transcription
CC factor (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Mdm2;
CC IsoId=P56950-1; Sequence=Displayed;
CC Name=Mdm2-alpha;
CC IsoId=P56950-2; Sequence=VSP_003206;
CC -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and
CC testicular tissues.
CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC Region II contains most of a central acidic region required for
CC interaction with ribosomal protein L5 and a putative C4-type zinc
CC finger. The RING finger domain which coordinates two molecules of
CC zinc interacts specifically with RNA whether or not zinc is
CC present and mediates the hetero-oligomerization with MDM4. It is
CC also essential for its ubiquitin ligase E3 activity toward p53 and
CC itself (By similarity).
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SWIB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF100705; AAF67833.1; -.
DR EMBL; AF322416; AAG42840.1; -.
DR HSP; Q9UMT8; 1YCR.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB.
DR InterPro; IPR001876; Znf_RanGDP.
DR InterPro; IPR001841; Znf_RanBP2_1; 1.
DR InterPro; IPR001841; Znf_RanBP2_1; 1.

DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01199; ZF_RANBP2_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Alternative splicing; Ligase; Metal-binding; Nuclear protein;
KW Ubiquitin conjugation pathway; Zinc; Zinc-finger.
FT DOMAIN 27 107 SWIB
FT DOMAIN 179 185 Nuclear localization signal (Potential).
FT DOMAIN 190 202 Nuclear export signal.
FT DOMAIN 210 304 ARF-binding.
FT DOMAIN 210 215 Poly-Ser.
FT DOMAIN 242 331 Region II.
FT DOMAIN 243 301 Asp/Glu-rich (acidic).
FT ZN_FING 299 328 RanBP2-type.
FT ZN_FING 434 475 RING-type.
FT DOMAIN 462 469 Nuclear localization signal
(Potential).
FT VARSPLIC 1 61 Missing (in isoform Mdm2-alpha).
FT CONFLICT 11 11 /FTid=VSP_003206.
FT CONFLICT 238 239 G->D (in Ref. 2).
SQ SEQUENCE 487 AA; 54696 MW; 60CDB470A32A8E69 CRC64;
Query Match 96.8%; Score 536; DB 1; Length 487;
Best Local Similarity 96.3%; Pred. No. 4.7e-49;
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKQYTTMKEVLYFGQYIMTKRLYDEKQHHVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKQYTTMKEVLYFGQYIMTKRLYDEKQHHV 76
Qy 61 CSNDLLGDLFGVPSFVKHKKIYTMIRNLVNVNQESSDSCTSVSEN 109
Db 77 CSNDLLGDLFGVPSFVKHKKIYTMIRNLVNVNQESSDSCTSVSEN 125
RESULT 6
Q9GMZ6 PRELIMINARY; PRT; 487 AA.
AC Q9GMZ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2.
GN Name=mdm2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Setoguchi A., Tsujimoto H.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB031276; BAB11975.1; -.
DR HSP; Q9UMT8; 1YCR.
DR GO; GO:0005730; C:nucleolus; ISS.
DR GO; GO:0005654; C:nucleoplasm; ISS.
DR GO; GO:0017163; F:negative regulator of basal transcription a...; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0000122; P:negative regulation of transcription from P...; ISS.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR InterPro; IPR001876; Znf_RanGDP.
DR InterPro; IPR001841; Znf_RanBP2_1.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01199; ZF_RANBP2_2; 1.

```
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 487 AA; 54724 MW; 34FCSC6A18D7744 CRC64;

Query Match
Best Local Similarity 96.8%; Score 536; DB 2; Length 487;
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTTMKVELFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTTMKVELFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRYRNLVVNQESSDSGTSVSEN 109
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRYRNLVVNQHPSPSGTSVSEN 125

RESULT 7
MDM2_HORSE
ID MDM2_HORSE STANDARD; PRT; 491 AA.
AC P56951;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN Name=MDM2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20218666; PubMed=10754200; DOI=10.1016/S0304-3835(99)00427-9;
RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA Argyle D.J.;
RT Cloning, sequence analysis and expression of the cDNAs encoding the
RT canine and equine homologues of the mouse double minute 2 (mdm2)
RT proto-oncogene."
RL Cancer Lett. 152:9-13 (2000).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis (By similarity).
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC similarity).
CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm (By similarity).
CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC Region II contains most of a central acidic region required for
CC interaction with ribosomal protein L5 and a putative C4-type zinc
CC finger. The RING finger domain which coordinates two molecules of
CC zinc interacts specifically with RNA whether or not zinc is
CC present and mediates the hetero-oligomerization with MDM4. It is
CC also essential for its ubiquitin ligase E3 activity toward p53 and
CC itself (By similarity).
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SWIB domain.

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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CC EMBL; AF121140; AAF28866.1; -.
DR HSP; Q9UMT8; 1YCR.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB.
DR InterPro; IPR001876; Znf_RanBP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF0641; Zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01199; ZF_RANBP2_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Ligase; Metal-binding; Nuclear protein; Ub1 conjugation pathway; Zinc;
KW Zinc-finger.
FT DOMAIN 27 107 SWIB.
FT DOMAIN 179 185 Nuclear localization signal (Potential).
FT DOMAIN 190 202 Nuclear export signal.
FT DOMAIN 210 304 ARF-binding.
FT DOMAIN 210 215 Poly-Ser.
FT DOMAIN 242 331 Region II.
FT DOMAIN 243 301 Asp/Glu-rich (acidic).
FT ZN_FING 299 328 RanBP2-type.
FT ZN_FING 438 479 RING-type.
FT DOMAIN 466 473 Nucleolar localization signal
(Potential).
SQ SEQUENCE 491 AA; 55279 MW; 641E033D5C1DEC39 CRC64;

Query Match 96.8%; Score 536; DB 1; Length 491;
Best Local Similarity 96.3%; Pred. No. 4.8e-49;
Matches 105; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTTMKVELFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTTMKVELFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGLDFGVPSFSVKEHRKIYTMIRYRNLVVNQESSDSGTSVSEN 109
Db 77 CSNDLLGLDFGVPSFSVKEHRKIYTMIRYRNLVVNQHPSPSGTSVSEN 125

RESULT 8
QYRZ8
ID QYRZ8 PRELIMINARY; PRT; 491 AA.
AC QYRZ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Double minute 2 protein MDM2.
GN Name=mdm2;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
SEQUENCE FROM N.A.
RA Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB099709; BAC78209.1; -.
DR GO; GO:0005730; C:nucleolus; ISS.
DR GO; GO:0005654; C:nucleoplasm; ISS.
DR GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:000122; P:negative regulation of transcription from P. . .; ISS.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR InterPro; IPR001876; Znf_RanBP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF0641; Zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
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DR PROSITE; PS50199; ZF_RANBP2_2; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 491 AA; 55433 MW; D93E25D638E88934 CRC64;

Query Match          96.2%; Score 533; DB 2; Length 491;
Best Local Similarity 95.4%; Pred. No. 1e-48; 2; Indels 0; Gaps 0;
Matches 104; Conservative 3; Mismatches 2;

QY 1 SQIPASEQETLVPRPPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
   |||
Db 17 SQMPASEQETLVPRPPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
   |||

QY 61 CSNDLLGDLFGVPSPSVKHKRIYTMVYRNLVVNNQSSSGTSVSEN 109
   |||
Db 77 CSNDLLGDLFGVPSPSVKHKRIYTMVYRNLVVNNQHEPSPSGTSVSEN 125
   |||

RESULT 9
Q8WYJ2 ID Q8WYJ2 PRELIMINARY; PRT; 436 AA.
AC Q8WYJ2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE MDM2 protein.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90);
RX MEDLINE=21248713; PubMed=11351297;
RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA Carpinelli P., Pierotti M.A., Pilotti S.;
RT "Analysis of the molecular species generated by MDM2 gene
RT amplification in liposarcomas.";
RL Int. J. Cancer 92:790-796(2001).
DR EMBL; AF092844; AAL40179.1; -.
DR HSP; Q9UNT8; 1YCR.
DR GO; GO:0005730; C:nucleolus; ISS.
DR GO; GO:0005654; C:nucleoplasm; ISS.
DR GO; GO:0007163; F:negative regulator of basal transcription a. . .; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:000122; P:negative regulation of transcription from P. . .; ISS.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS50199; ZF_RANBP2_2; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 436 AA; 49248 MW; 3C9F55E98BC4203A CRC64;

Query Match          89.9%; Score 498; DB 2; Length 436;
Best Local Similarity 93.3%; Pred. No. 5.2e-45;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
   |||
Db 17 SQIPASEQETLVPRPPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
   |||

QY 61 CSNDLLGDLFGVPSPSVKHKRIYTMVYRNLVVNNQSSSGTS 105
   |||
Db 77 CSNDLLGDLFGVPSPSVKHKRIYTMVYRNLVVNNQSENSDLS 121
   |||

RESULT 10
MDM2_MOUSE ID MDM2_MOUSE STANDARD; PRT; 489 AA.
AC P23804; Q61040; Q64330;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
GN Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX MEDLINE=91224107; PubMed=2026149;
RA Fatharzadeh S.S., Trusko S.P., George D.L.;
RT "Tumorigenic potential associated with enhanced expression of a gene
RT that is amplified in a mouse tumor cell line.";
RL EMBO J. 10:1565-1569(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX STRAIN=129/SV;
RX MEDLINE=97074674; PubMed=8917101; DOI=10.1016/0378-1119(96)00151-5;
RA Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA Donehower L.A., Bradley A.;
RT "Genomic organization of the mouse double minute 2 gene.";
RL Gene 175:209-213(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX STRAIN=129/SV;
RX MEDLINE=96299630; PubMed=8660994; DOI=10.1006/geno.1996.0210;
RA de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA Saucedo L.J., Myers C.D., Perry M.E.;
RT "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT ultraviolet light.";
RL J. Biol. Chem. 274:8161-8168(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX MEDLINE=99175199; PubMed=10075719; DOI=10.1074/jbc.274.12.8161;
RA Saucedo L.J., Myers C.D., Perry M.E.;
RT "The organization and expression of the mdm2 gene.";
RL Genomics 33:352-357(1996).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX MEDLINE=20180080; PubMed=10713175;
RX DOI=10.1128/MCB.20.7.2517-2528.2000;
RA Weber J.D., Kuo M.-L., Bothner B., DiGiarmarino E.L., Kriwacki R.W.,
RA Rousset M.F., Sherr C.J.;
RT "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT localization of the complex.";
RL Mol. Cell. Biol. 20:2517-2528(2000).
RN [6]
RP PHOSPHORYLATION BY ATM.
RX MEDLINE=20079591; PubMed=10611322; DOI=10.1073/pnas.96.26.14973;
RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT in response to DNA damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC -1- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis.
CC -1- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC -1- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor.
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm. Interaction with ARF(P14)
CC results in the localization of both proteins to the nucleolus. The
CC nucleolar localization signals in both ARF(P14) and MDM2 may be
CC necessary to allow efficient nucleolar localization of both
CC proteins.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Mdm2-p90;
CC IsoId=P23804-1; Sequence=Displayed;

```


Note-Isoform Mdm2-p76 can also be produced by alternative initiation at Met-50 of isoform Mdm2-p90, but is produced more efficiently by alternative splicing;
Name=Mdm2-p76;
IsoId=P23804-2; Sequence=VSP_003215;
Note=Does not bind to p53;
Event=Alternative initiation;
Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are produced by alternative initiation at Met-1 and Met-50. Isoform Mdm2-p76 is produced more efficiently by alternative splicing;
-!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout embryo development and in adult tissues. Mdm2-p90 is much more abundant than Mdm2-p76 in testis, brain, heart, and kidney, but in the thymus, spleen, and intestine, the levels of the MDM2 proteins are roughly equivalent.
-!- INDUCTION: By UV light.
-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself.
-!- PTM: Phosphorylated in response to ionizing radiation in an ATM-dependent manner.
-!- DISEASE: The gene for this protein is amplified in a mouse tumor cell line.
-!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
-!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 SWIB domain.

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DR EMBL; X58876; CAA41684.1; -;
DR EMBL; U40145; AAA91167.1; -;
DR EMBL; U47944; AAB09030.1; -;
DR EMBL; U47935; AAB09030.1; JOINED.
DR EMBL; U47936; AAB09030.1; JOINED.
DR EMBL; U47937; AAB09030.1; JOINED.
DR EMBL; U47938; AAB09030.1; JOINED.
DR EMBL; U47939; AAB09030.1; JOINED.
DR EMBL; U47940; AAB09030.1; JOINED.
DR EMBL; U47941; AAB09030.1; JOINED.
DR EMBL; U47942; AAB09030.1; JOINED.
DR EMBL; U47943; AAB09030.1; JOINED.
DR EMBL; U47934; AAB09031.1; -;
DR PIR; S15349; S15349.
DR HSSP; Q9UMT8; 1YCR.
DR MGD; MGI:96952; Mdm2.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR GO; GO:0030163; P:protein catabolism; IDA.
DR GO; GO:0016567; P:protein ubiquitination; IDA.
DR GO; GO:0007089; P:traversing start control point of mitotic c. .; IDA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB.
DR InterPro; IPR001876; Znf_RanGDP.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01199; ZF_RANBP2_2; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Alternative initiation; Alternation; Ligase; Metal-binding;
KW Nuclear protein; Phosphorylation; Proto-oncogene;
KW Ub1 conjugation pathway; Zinc; Zinc-finger.
FT CHAIN 1 489
FT Ubiqutin-protein ligase E3 Mdm2, isoform Mdm2-p90.
FT CHAIN 50 489
FT Ubiquitin-protein ligase E3 Mdm2, isoform Mdm2-p76.
FT INIT MET 50 50
FT DOMAIN 27 107
FT DOMAIN 176 182
FT DOMAIN 183 195
FT DOMAIN 203 213
FT DOMAIN 208 302
FT DOMAIN 220 329
FT DOMAIN 221 299
FT ZN_FING 297 326
FT ZN_FING 436 477
FT DOMAIN 464 471
FT VARSPPLIC 1 49
FT Missing (in isoform Mdm2-p76).
FT CONFLICT 203 203
FT CONFLICT 419 419
FT CONFLICT 486 486
SQ SEQUENCE 489 AA; 54543 MW; 4ABF489E92038DF4 CRC64;
Query Match 88.2%; Score 488.5; DB 1; Length 489;
Best Local Similarity 87.2%; Pred. No. 6.2e-44;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;
QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQNDYTKWKEVLYLQGYIMTKRLYDEKQOHVH 60
Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQNDYTKWKEVLYLQGYIMTKRLYDEKQOHVY 76
QY 61 CSNDLLGDLGVPSFVKEHRIYIMYRNLYVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLGVPSFVKEHRIYIMYRNLYVNVNQESSDSGTSVSEN 122
RESULT 11
QY1XK7 PRELIMINARY; PRT; 489 AA.
AC QY1XK7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011p22 product:transformed mouse 3T3 cell double minute 2, full insert sequence (transformed mouse 3T3 cell double minute 2, musculus 2 days neonate thymic cells cDNA, RIKEN full-length enriched library, clone:E43022B10 product:transformed mouse 3T3 cell double minute 2, full insert sequence).
GN Name=Mdm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=lung, and Thymus;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=lung, and Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).

DR Pfam; PF02201; SWIB; 1.
 FT NON_TER 118 118
 SQ SEQUENCE 118 AA; 13536 MW; D7A4DBAA83D8841B CRC64;

Query Match 85.0%; Score 471; DB 2; Length 118;
 Best Local Similarity 98.9%; Pred. No. 9.4e-43;
 Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60
 DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNVLV 93
 DB 77 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNVLV 109

RESULT 13
 MDM2_MESAU STANDARD; PRT; 466 AA.
 ID MDM2_MESAU
 AC Q60524;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).
 GN Name=MDM2;
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95300112; PubMed=7780969;
 RA Chang K.W., Leoni S., Mangold K.A., Huchak S., Scarpelli D.G.;
 RT "Multiple genetic alterations in hamster pancreatic ductal adenocarcinomas";
 RL Cancer Res. 55:2560-2568(1995).
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain.
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity).
 CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).
 CC -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein BP300 and the E2F1 transcription factor (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).
 CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).
 CC -!- DISEASE: The gene for this protein is overexpressed in some tumors.
 CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
 CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- SIMILARITY: Contains 1 SWIB domain.
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 CC -----
 CC EMBL; U10982; AAC52425.1; -.
 DR HSSP; Q9UMT8; 1YCR.
 DR InterPro; IPR010984; MDM2.
 DR InterPro; IPR003121; SWIB.
 DR InterPro; IPR001876; Znf_RangDP.
 DR InterPro; IPR001841; Znf_Ring.
 DR Pfam; PF02201; SWIB; 1.
 DR Pfam; PF00641; zf-RanBP; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01358; ZF_RANBP2_1; 1.
 DR PROSITE; PS01359; ZF_RANBP2_2; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00518; ZF_RING_2; 1.
 KW Ligase; Metal-binding; Nuclear protein; Proto-oncogene;
 KW Ub1 conjugation pathway; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT DOMAIN 19 98 SWIB.
 FT DOMAIN 169 175 Nuclear localization signal (Potential).
 FT DOMAIN 176 188 Nuclear export signal.
 FT DOMAIN 196 201 Poly-Ser.
 FT DOMAIN 196 290 ARF-binding.
 FT DOMAIN 228 317 Region II.
 FT DOMAIN 209 314 Asp/Glu-rich (acidic).
 FT ZN_FING 285 314 RanBP2-type.
 FT ZN_FING 419 460 RING-type.
 FT DOMAIN 447 454 Nucleolar localization signal (Potential).
 FT NON_TER 466 466
 SQ SEQUENCE 466 AA; 52390 MW; 78A3042163C5F939 CRC64;

Query Match 83.8%; Score 464.5; DB 1; Length 466;
 Best Local Similarity 85.3%; Pred. No. 2.3e-41;
 Matches 93; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60
 DB 9 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVY 67

QY 61 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNVLV 109
 DB 68 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNVLV 116

RESULT 14
 Q9PVL2
 ID Q9PVL2 PRELIMINARY; PRT; 325 AA.
 AC Q9PVL2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MDM2 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LaFleur D.A., Foster D.N.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005045; AAF04192.1; -.
 DR HSSP; Q9UMT8; 1YCR.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR InterPro; IPR010984; MDM2.
 DR InterPro; IPR003121; SWIB_MDM2.
 DR InterPro; IPR001876; Znf_RangDP.
 DR Pfam; PF02201; SWIB; 1.
 DR Pfam; PF00641; zf-RanBP; 1.
 DR PROSITE; PS01358; ZF_RANBP2_1; 1.

Search completed: February 16, 2005, 08:24:05
Job time : 172 secs